

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 18:29:37 ; Search time 9967.36 Seconds

(Without alignments)  
42.201 Million cell updates/sec

Title: US-09-631-709-5

Perfect score: 1 caagaattctcatgttgacagct 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 17159718 seqs, 876320856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	24	100.0	24	24 US-09-631-709-5	Sequence 5, Appl1
2	24	100.0	29	1 PCT-US00-27212-1	Sequence 1, Appl1
3	24	100.0	57	15 US-09-132-231-13	Sequence 13, Appl1
4	24	100.0	4752	6 US-08-299-0922A-7	Sequence 7, Appl1
5	24	100.0	4752	12 US-08-819-723-7	Sequence 7, Appl1
6	24	100.0	4754	6 US-08-299-0922A-5	Sequence 5, Appl1
7	24	100.0	4754	12 US-08-819-723-5	Sequence 5, Appl1
8	24	100.0	5005	7 US-08-398-139B-60	Sequence 60, Appl1
9	24	100.0	6264	19 US-09-517-466-151	Sequence 151, App
10	24	100.0	6354	19 US-09-517-466-145	Sequence 145, App
11	24	100.0	6422	19 US-09-517-466-142	Sequence 142, App
12	24	100.0	6652	19 US-09-517-466-153	Sequence 153, App
13	24	100.0	6675	19 US-09-517-466-144	Sequence 144, App
14	24	100.0	6961	19 US-09-517-466-152	Sequence 152, App
15	24	100.0	7013	19 US-09-517-466-143	Sequence 143, App
16	24	100.0	7114	19 US-09-517-466-181	Sequence 181, App
17	24	100.0	8540	8 US-08-487-283A-4	Sequence 4, Appl1
18	24	100.0	8540	8 US-08-487-283A-6	Sequence 6, Appl1
19	24	100.0	8575	6 US-08-541-572-6	Sequence 6, Appl1
20	24	100.0	8932	6 US-08-252-493A-8	Sequence 8, Appl1
21	24	100.0	10332	18 US-09-423-838-13	Sequence 13, Appl1
22	24	100.0	10380	15 US-09-040-961-1	Sequence 1, Appl1
23	24	100.0	10380	15 US-09-130-115-1	Sequence 1, Appl1
24	24	100.0	11265	18 US-09-402-020-1	Sequence 1, Appl1
25	24	100.0	11265	18 US-09-471-669-48	Sequence 48, Appl1
26	24	100.0	16080	19 US-09-501-708-48	Sequence 48, Appl1
27	24	100.0	16080	29 US-09-723-739-48	Sequence 48, Appl1
28	24	100.0	16080	29 US-09-724-566-48	Sequence 48, Appl1
29	24	100.0	16080	29 US-09-724-568-48	Sequence 48, Appl1
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31	24	100.0	16080	29 US-09-724-571-48	Sequence 48, Appl1
32	24	100.0	16080	29 US-09-721-479B-10	Sequence 10, Appl1
33	24	100.0	16080	29 US-09-721-479B-8	Sequence 8, Appl1
34	24	100.0	16080	29 US-09-721-479B-12	Sequence 12, Appl1
35	24	100.0	16080	29 US-09-721-479B-16	Sequence 16, Appl1
36	24	100.0	16080	29 US-09-721-479B-18	Sequence 18, Appl1
37	24	100.0	16080	29 US-09-721-479B-14	Sequence 14, Appl1
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43	24	100.0	16080	29 US-09-721-479B-14	Sequence 14, Appl1

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42 23 95.8 5076 32 US-09-902-537-8 Sequence 8, Appl  
43 23 95.8 6989 1 PCT-US01-21701-11 Sequence 11, Appl  
44 23 95.8 6989 32 US-09-902-537-11 Sequence 11, Appl  
45 23 95.8 12379 32 US-09-902-537-14 Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-09-631-709-5  
; Sequence 5, Application US/09631709  
; GENERAL INFORMATION:  
; APPLICANT: KYOMA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: PROCESS FOR PRODUCING GDP-FUCOSE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/631,709  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver.2.0  
; SEQ ID NO: 5  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-631-709-5

Query Match 100.0%; Score 24; DB 24; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0;

QY 1 caagaattcctcattgttgacagct 24  
DB 1 caagaattcctcattgttgacagct 24

RESULT 2  
PCT-US00-27212-1  
; Sequence 1, Application PC/TUS0027212  
; GENERAL INFORMATION:  
; APPLICANT: NOINAR-KIMBER, KATHERINE  
; APPLICANT: TOYOZUMI, TAKANE  
; TITLE OF INVENTION: REPLICATION SELECTIVE ADENOVIRUSES FOR USE IN CANCER  
; TITLE OF INVENTION: THERAPY  
; FILE REFERENCE: 22253-66146  
; CURRENT APPLICATION NUMBER: PCT/US00/27212  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/157,224  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCR generated  
PCT-US00-27212-1

Query Match 100.0%; Score 24; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0;

QY 1 caagaattcctcattgttgacagct 24  
DB 4 caagaattcctcattgttgacagct 27

RESULT 3

US-09-132-231-13  
; Sequence 13, Application US/09132231A  
; GENERAL INFORMATION:  
; APPLICANT: HORWITZ, Marshall S.  
; APPLICANT: LOEB, Lawrence A.  
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH  
; FILE REFERENCE: 032425-001  
; CURRENT APPLICATION NUMBER: US/09/132,231A  
; PRIOR FILING DATE: 1998-08-11  
; PRIOR APPLICATION NUMBER: US 08/316,415  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO: 13  
; LENGTH: 57  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-09-132-231-13

Query Match 100.0%; Score 24; DB 15; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0;

QY 1 caagaattcctcattgttgacagct 24  
DB 1 caagaattcctcattgttgacagct 24

RESULT 4  
US-08-299-092A-7  
; Sequence 7, Application US/08299092A  
; GENERAL INFORMATION:  
; APPLICANT: Coughlin, Richard T.  
; APPLICANT: Ma, Jinneng  
; TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria  
; TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter  
; TITLE OF INVENTION: Assay for Borrelia Activity of Antisera  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,092A  
; FILING DATE: 02-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/025,379  
; FILING DATE: 26-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fleisher, Raz E.  
; REGISTRATION NUMBER: 34,331  
; REFERENCE/DOCKET NUMBER: 0614,1080002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4752 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..939  
US-08-299-092A-7

Query Match 100.0%; Score 24; DB 6; Length 4752;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgtttgacgct 24  
Db 4045 CAAGAATTCATGTTGACAGCT 4068

RESULT 5  
US-08-819-723-7  
Sequence 7, Application US/08819723  
GENERAL INFORMATION:  
APPLICANT: Coughlin, Richard T.  
APPLICANT: Ma, Jiansheng  
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria  
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,723  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/299,092  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Flesher, Raz E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 1673,1080003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4752 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..939  
US-08-819-723-7

Query Match 100.0%; Score 24; DB 12; Length 4752;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgtttgacgct 24  
Db 4045 CAAGAATTCATGTTGACAGCT 4068

RESULT 6  
US-08-299-092A-5  
Sequence 5, Application US/08299092A  
GENERAL INFORMATION:  
APPLICANT: Coughlin, Richard T.  
APPLICANT: Ma, Jiansheng  
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria  
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299,092A  
FILING DATE: 02-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/025,379  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Flesher, Raz E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 0614,1080002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..870  
US-08-299-092A-5

Query Match 100.0%; Score 24; DB 6; Length 4754;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgtttgacgct 24  
Db 4047 CAAGAATTCATGTTGACAGCT 4070

RESULT 7  
US-08-819-723-5  
Sequence 5, Application US/08819723  
GENERAL INFORMATION:  
APPLICANT: Coughlin, Richard T.  
APPLICANT: Ma, Jiansheng  
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria  
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington

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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,723
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,092
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 1673.1080003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..870
US-08-819-723-5

Query Match      100.0%; Score 24; DB 12; Length 4754;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgaacgt 24
Db 4047 CAAGAATCTCATGTGACAGCT 4070

RESULT 8
US-08-398-139B-60/C
GENERAL INFORMATION:
APPLICANT: Anderson, Carl W.
TITLE OF INVENTION: DNA-PK Assay
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
STREET: Building 902C, P.O. Box 5000
CITY: Upton
STATE: New York
COUNTRY: USA
ZIP: 11973-5000
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM XT compatible
OPERATING SYSTEM: MS DOS Ver. 6.0
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,139B
FILING DATE: 3-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132,284
FILING DATE: 6-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
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REFERENCE/DOCKET NUMBER: AUI 94-27
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 5005 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-398-139B-60

Query Match      100.0%; Score 24; DB 7; Length 5005;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgaacgt 24
Db 385 CAAGAATCTCATGTGACAGCT 362

RESULT 9
US-09-517-466-151/C
GENERAL INFORMATION:
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
APPLICANT: Cheo, David
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
FILE REFERENCE: 0942.4680003
CURRENT FILING DATE: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 151
LENGTH: 6264
TYPE: DNA
ORGANISM: PDEST23
FEATURE:
NAME/KEY: gene
LOCATION: (161)..(285)
OTHER INFORMATION: attR1
NAME/KEY: gene
LOCATION: (394)..(1053)
OTHER INFORMATION: cmr
NAME/KEY: gene
LOCATION: (1173)..(1257)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1395)..(1700)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (1741)..(1865)
OTHER INFORMATION: attR2
NAME/KEY: gene
LOCATION: (1883)..(1911)
OTHER INFORMATION: his6
NAME/KEY: gene
LOCATION: (2574)..(3434)
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LOCATION: (3583)..(4222)
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Query Match 100.0%; Score 24; DB 19; Length 6264;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
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DB 2371 CAAGAATTCTCATGTTTGACAGCT 2348

RESULT 10  
US-09-517-466-145/C

Sequence 145, Application US/09517466  
GENERAL INFORMATION:  
APPLICANT: Hartley, James  
APPLICANT: Brasch, Michael  
APPLICANT: Temple, Gary  
APPLICANT: Cheo, David  
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of  
FILE REFERENCE: 0942.4680003  
CURRENT APPLICATION NUMBER: US/09/517,466  
CURRENT FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/122,389  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/126,049  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/136,744  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 184  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 145  
LENGTH: 6354  
TYPE: DNA  
ORGANISM: pDEST17  
FEATURE:  
NAME/KEY: gene  
LOCATION: (134)..(258)  
OTHER INFORMATION: attR1  
NAME/KEY: gene  
LOCATION: (367)..(1026)  
OTHER INFORMATION: Cmr  
NAME/KEY: gene  
LOCATION: (1146)..(1230)  
OTHER INFORMATION: Inactivated ccda  
NAME/KEY: gene  
LOCATION: (1368)..(1673)  
OTHER INFORMATION: ccdb  
NAME/KEY: gene  
LOCATION: (1714)..(1838)  
OTHER INFORMATION: attR2  
NAME/KEY: gene  
LOCATION: (2564)..(3421)  
OTHER INFORMATION: ampr  
US-09-517-466-145

Query Match 100.0%; Score 24; DB 19; Length 6354;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
|||||  
DB 2361 CAAGAATTCTCATGTTTGACAGCT 2338

RESULT 11  
US-09-517-466-142/C

Sequence 142, Application US/09517466  
GENERAL INFORMATION:  
APPLICANT: Hartley, James  
APPLICANT: Brasch, Michael  
APPLICANT: Temple, Gary  
APPLICANT: Cheo, David

TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning  
FILE REFERENCE: 0942.4680003  
CURRENT APPLICATION NUMBER: US/09/517,466  
CURRENT FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/122,389  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/126,049  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/136,744  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 184  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 142  
LENGTH: 6422  
TYPE: DNA  
ORGANISM: pDEST14  
FEATURE:  
NAME/KEY: gene  
LOCATION: (61)..(185)  
OTHER INFORMATION: attR1  
NAME/KEY: gene  
LOCATION: (435)..(1094)  
OTHER INFORMATION: Cmr  
NAME/KEY: gene  
LOCATION: (1214)..(1298)  
OTHER INFORMATION: Inactivated ccda  
NAME/KEY: gene  
LOCATION: (1436)..(1741)  
OTHER INFORMATION: ccdb  
NAME/KEY: gene  
LOCATION: (1782)..(1906)  
OTHER INFORMATION: attR2  
NAME/KEY: gene  
LOCATION: (2632)..(3489)  
OTHER INFORMATION: ampr  
US-09-517-466-142

Query Match 100.0%; Score 24; DB 19; Length 6422;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
|||||  
DB 2429 CAAGAATTCTCATGTTTGACAGCT 2406

RESULT 12  
US-09-517-466-153/C

Sequence 153, Application US/09517466  
GENERAL INFORMATION:  
APPLICANT: Hartley, James  
APPLICANT: Brasch, Michael  
APPLICANT: Temple, Gary  
APPLICANT: Cheo, David  
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning  
FILE REFERENCE: 0942.4680003  
CURRENT APPLICATION NUMBER: US/09/517,466  
CURRENT FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/122,389  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/126,049  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/136,744  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 184  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 153  
LENGTH: 6652  
TYPE: DNA  
ORGANISM: pDEST25

Fri Dec 14 09:21:22 2001

us-09-631-709-5.inpm

Page 6

```
FEATURE:
NAME/KEY: gene
LOCATION: (720)..(844)
OTHER INFORMATION: attR1
NAME/KEY: gene
LOCATION: (953)..(1612)
OTHER INFORMATION: CMR
NAME/KEY: gene
LOCATION: (1732)..(1816)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1954)..(2259)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (2300)..(2424)
OTHER INFORMATION: attR2
NAME/KEY: gene
LOCATION: (2432)..(2794)
OTHER INFORMATION: trx
US-09-517-466-153
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Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6652;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
DB 3318 CAAGAATTCATGTTGACAGCT 3295
```

```
RESULT 13
US-09-517-466-144/c
Sequence 144, Application US/09517466
GENERAL INFORMATION:
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of
FILE REFERENCE: 0942.4680003
CURRENT APPLICATION NUMBER: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 6675
TYPE: DNA
ORGANISM: pDEST16
FEATURE:
NAME/KEY: gene
LOCATION: (104)..(457)
OTHER INFORMATION: trx
NAME/KEY: gene
LOCATION: (461)..(585)
OTHER INFORMATION: attR1
NAME/KEY: gene
LOCATION: (594)..(1353)
OTHER INFORMATION: CMR
NAME/KEY: gene
LOCATION: (1473)..(1557)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1695)..(2000)
OTHER INFORMATION: ccdb
NAME/KEY: gene
```

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LOCATION: (2041)..(2165)
OTHER INFORMATION: attR2
US-09-517-466-144
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Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6675;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
DB 2688 CAAGAATTCATGTTGACAGCT 2665
```

```
RESULT 14
US-09-517-466-152/c
Sequence 152, Application US/09517466
GENERAL INFORMATION:
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
FILE REFERENCE: 0942.4680003
CURRENT APPLICATION NUMBER: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 152
LENGTH: 6961
TYPE: DNA
ORGANISM: pDEST24
FEATURE:
NAME/KEY: gene
LOCATION: (71)..(195)
OTHER INFORMATION: attR1
NAME/KEY: gene
LOCATION: (304)..(963)
OTHER INFORMATION: CMR
NAME/KEY: gene
LOCATION: (1083)..(1167)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1305)..(1610)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (1651)..(1775)
OTHER INFORMATION: attR2
NAME/KEY: gene
LOCATION: (1783)..(2451)
OTHER INFORMATION: GST
NAME/KEY: gene
LOCATION: (3181)..(4041)
OTHER INFORMATION: ampr
NAME/KEY: gene
LOCATION: (4190)..(4829)
OTHER INFORMATION: ori
US-09-517-466-152
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6961;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
```

Db 2978 CAAGATTCTCATGTTCACAGCT 2955

RESULT 15

US-09-517-466-143/C  
Sequence 143, Application US/09517466

GENERAL INFORMATION:

APPLICANT: Hartley, James  
APPLICANT: Brasch, Michael  
APPLICANT: Temple, Gary

APPLICANT: Cheo, David

TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of

FILE REFERENCE: 0942.4680003

CURRENT APPLICATION NUMBER: US/09/517,466

PRIOR APPLICATION NUMBER: US 60/122,389

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: US 60/126,049

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: US 60/136,744

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.0

SEQ ID NO 143

LENGTH: 7013

TYPE: DNA

ORGANISM: pDEST15

FEATURE:

NAME/KEY: gene  
LOCATION: (108)..(776)

OTHER INFORMATION: GST

NAME/KEY: gene

LOCATION: (792)..(916)

OTHER INFORMATION: atcR1

NAME/KEY: gene

LOCATION: (1025)..(1537)

OTHER INFORMATION: CMR

NAME/KEY: gene

LOCATION: (1804)..(1888)

OTHER INFORMATION: Inactivated ccda

NAME/KEY: gene

LOCATION: (2026)..(2331)

OTHER INFORMATION: ccdb

NAME/KEY: gene

LOCATION: (2372)..(2496)

OTHER INFORMATION: atcR2

NAME/KEY: gene

LOCATION: (3233)..(4093)

OTHER INFORMATION: ampr

US-09-517-466-143

Query Match 100.0%; Score 24; DB 19; Length 7013;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgttcacagct 24  
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Db 3030 CAAGATTCTCATGTTCACAGCT 3007

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Job time: 18173 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 13:32:30 : Search time 176.03 Seconds  
(without alignments)  
30.878 Million cell updates/sec

Title: US-09-631-709-5

Perfect score: 24

Sequence: 1 caagattctcatgtttgacagct 24

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 11338999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued\_Patents\_NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	35	1	US-07-985-690A-9	Sequence 9, Appl1
2	24	100.0	55	1	US-08-441-116-1	Sequence 1, Appl1
3	24	100.0	3918	2	US-08-495-500-2	Sequence 2, Appl1
4	24	100.0	5552	3	US-08-155-888-1	Sequence 1, Appl1
5	24	100.0	6623	2	US-08-244-434-36	Sequence 36, Appl1
6	24	100.0	6630	2	US-08-244-434-37	Sequence 37, Appl1
7	24	100.0	6727	2	US-08-125-462-2	Sequence 2, Appl1
8	24	100.0	6727	2	US-08-891-848-2	Sequence 2, Appl1
9	24	100.0	6799	2	US-08-125-462-5	Sequence 5, Appl1
10	24	100.0	6799	2	US-08-891-848-5	Sequence 5, Appl1
11	24	100.0	8540	5	PCT-US96-05611A-12	Sequence 12, Appl1
12	24	100.0	8575	5	PCT-US97-08258-6	Sequence 6, Appl1
13	24	100.0	8932	2	US-08-252-493C-8	Sequence 8, Appl1
14	24	100.0	8932	3	US-09-276-197-8	Sequence 8, Appl1
15	24	100.0	11616	1	US-08-196-259-2	Sequence 2, Appl1
16	24	100.0	34303	2	US-08-735-609-4	Sequence 4, Appl1
17	24	100.0	34303	2	US-08-735-609-4	Sequence 4, Appl1
18	24	100.0	34303	3	US-09-315-372-4	Sequence 4, Appl1
19	24	100.0	34303	3	US-09-244-752-4	Sequence 4, Appl1
20	24	100.0	34303	3	US-09-245-497-4	Sequence 4, Appl1
21	23	95.8	8501	4	US-08-793-900-1	Sequence 1, Appl1
22	22.4	93.3	6166	4	US-08-591-632-51	Sequence 51, Appl1
23	22.4	93.3	8157	1	US-08-358-160-65	Sequence 65, Appl1
24	22.4	93.3	8584	1	US-08-358-160-66	Sequence 66, Appl1
25	22.4	93.3	8590	1	US-08-358-160-70	Sequence 70, Appl1
26	22	91.7	7641	1	US-07-924-028A-5	Sequence 5, Appl1
27	21.4	89.2	1738	1	US-07-971-160-9	Sequence 9, Appl1

28	21.4	89.2	1738	1	US-08-336-241-9	Sequence 9, Appl1
29	21.4	89.2	1738	2	US-08-465-273-9	Sequence 9, Appl1
30	21.4	89.2	1738	2	US-09-119-024-9	Sequence 9, Appl1
31	21.4	89.2	1738	2	US-08-417-226-9	Sequence 9, Appl1
32	21.4	89.2	1738	4	US-09-196-131-9	Sequence 15, Appl1
33	21.4	89.2	10596	1	US-07-884-811-15	Sequence 15, Appl1
34	21.4	89.2	10596	1	US-07-885-971-15	Sequence 15, Appl1
35	21.4	89.2	10596	1	US-08-087-783A-15	Sequence 15, Appl1
36	21.4	89.2	10596	2	US-08-194-088B-15	Sequence 15, Appl1
37	21.4	89.2	10596	2	US-08-194-087-15	Sequence 15, Appl1
38	21.4	89.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl1
39	21	87.5	31	4	US-08-416-544B-14	Sequence 14, Appl1
40	21	87.5	1130	2	US-08-613-965-1	Sequence 1, Appl1
41	21	87.5	1130	2	US-08-918-966-1	Sequence 1, Appl1
42	21	87.5	1130	3	US-08-921-655-1	Sequence 1, Appl1
43	21	87.5	5249	1	US-08-688-649-3	Sequence 3, Appl1
44	21	87.5	5249	1	US-08-688-649-4	Sequence 4, Appl1
45	21	87.5	7859	1	US-07-854-596B-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-07-985-690A-9  
: Sequence 9, Application US/07985690A  
: Patent No. 5376545  
: GENERAL INFORMATION:  
: APPLICANT: Yagasaki, Makoto  
: APPLICANT: Ishino, Shuichi  
: APPLICANT: Iwata, Kazuhisa  
: APPLICANT: Azuma, Masaki  
: APPLICANT: Teshiba, Sadao  
: APPLICANT: Hasegawa, Masaru  
: APPLICANT: Yamaguchi, Kazuo  
: APPLICANT: Yano, Keiichi  
: APPLICANT: Yokoo, Yoshiharu  
: APPLICANT: Hashimoto, Yukio  
: TITLE OF INVENTION: DNA CODING FOR URICASE AND PROCESS FOR  
: TITLE OF INVENTION: PRODUCING URICASE  
: NUMBER OF SEQUENCES: 13  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS  
: STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.  
: City: Washington,  
: STATE: D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20006  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage  
: COMPUTER: NEC PC-9801 Series  
: OPERATING SYSTEM: MS-DOS Ver3.30 or Later  
: SOFTWARE: PATENT AID  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/985,690A  
: FILING DATE: 19921203  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP91/320525  
: FILING DATE: 04-DEC-1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Terry, David T.  
: REGISTRATION NUMBER: 20178  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 202-828-0300  
: TELEFAX: 202-828-0380  
: TELEX: 440280  
: INFORMATION FOR SEQ ID NO: 9:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 35 base pairs  
: TYPE: NUCLEIC ACID  
: STRANDEDNESS: single  
: TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid  
SYNTHETIC DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-985-690A-9

Query Match 100.0%; Score 24; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24  
|||||  
DB 4 CAAGAATTCATGTTTGACAGCT 27

## RESULT 2

US-08-441-116-1  
Sequence 1, Application US/08441116  
Patent No. 5641764  
GENERAL INFORMATION:  
APPLICANT: Martin, Roger F.  
TITLE OF INVENTION: HALOGENATED DNA LIGAND  
TITLE OF INVENTION: RADIOSENSITISERS FOR CANCER THERAPY  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington, D.C.  
COUNTRY: United States of America  
ZIP: 22037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.116  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,588  
FILING DATE: 30-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kit, Gordon  
REGISTRATION NUMBER: 30,764  
REFERENCE/DOCKET NUMBER: Q27431  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 393-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-441-116-1

Query Match 100.0%; Score 24; DB 1; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24  
|||||  
DB 17 CAAGAATTCATGTTTGACAGCT 40

US-08-495-500-2  
Sequence 2, Application US/08495500  
Patent No. 5962222

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: Protein fusions for the translocation of  
TITLE OF INVENTION: Apo-protein into the periplasmic space  
NUMBER OF SEQUENCES: 3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/495,500  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GR 9301553.5  
FILING DATE: 27-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 93/044,001  
FILING DATE: 27-JAN-1994  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-495-500-2

Query Match 100.0%; Score 24; DB 2; Length 3918;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24  
|||||  
DB 2689 CAAGAATTCATGTTTGACAGCT 2712

## RESULT 4

US-08-155-888-1/c  
Sequence 1, Application US/08155888  
Patent No. 6066623  
GENERAL INFORMATION:  
APPLICANT: Hoffman, Stephen L.  
APPLICANT: Hedstrom, Richard C.  
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE  
TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR  
DELIVERING POLYNUCLEOTIDE VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Naval Medical Res. & Dev. Cnd.  
STREET: Bldg. 1, T-12 8901 Wisconsin Ave.  
CITY: Bethesda  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20889-5606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/155,888  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spevack, A. David

REGISTRATION NUMBER: 24,743  
REFERENCE/DOCKET NUMBER: N.C. 75,851  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 295-6759  
TELEFAX: (202) 295-1022  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5552 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: promoter  
LOCATION: 1..755  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /function="promoter"  
OTHER INFORMATION: /evidence=EXPERIMENTAL  
OTHER INFORMATION: /label=CMV-IE  
OTHER INFORMATION: /note="this feature acts as a promoter for any  
OTHER INFORMATION: downstream DNA sequence."  
OTHER INFORMATION: /citation=(12)]  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 933..2367  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /codon\_start=933  
OTHER INFORMATION: /function="protein protective against malaria"  
OTHER INFORMATION: /product="protein"  
OTHER INFORMATION: /evidence=EXPERIMENTAL  
OTHER INFORMATION: /number=1  
OTHER INFORMATION: /label=IL2-CSP  
OTHER INFORMATION: /citation=(11)]  
PUBLICATION INFORMATION:  
AUTHORS: Sedegah, Martha  
AUTHORS: Hedstrom, Richard C.  
AUTHORS: Hoffman, Stephen L.  
TITLE: Vaccination with Plasmodium yoelii CS protein  
TITLE: plasmid DNA protects against malaria  
JOURNAL: Science  
PUBLICATION INFORMATION:  
AUTHORS: Cullen, Bryan R.  
TITLE: TRANS-ACTIVATION OF HUMAN IMMUNODEFICIENCY  
TITLE: VIRUS OCCURS VIA A BIMODAL MECHANISM  
JOURNAL: CELL  
VOLUME: 46  
PAGES: 973-982  
DATE: 26 SEP-1986  
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4732  
US-08-155-888-1

Query Match 100.0%; Score 24; DB 3; Length 5552;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcctggttgacgct 24  
|||||

Db 3259 CAAGAATTCATGTTGACAGCT 3236

RESULT 5  
US-08-244-434-36  
Sequence 36, Application US/08244434  
Patent No. 5854004  
GENERAL INFORMATION:  
APPLICANT: Czeruliofsky, A.P.  
APPLICANT: Himmler, A.  
APPLICANT: Stralowa, C.  
APPLICANT: Weyer, U.  
APPLICANT: Lamche, H.  
APPLICANT: Sch fer, R.

TITLE OF INVENTION: Process for Screening Substances Capable of  
TITLE OF INVENTION: Modulating a Receptor-Dependent Cellular Signal  
TITLE OF INVENTION: Transmission Path  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,434  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/92/02718  
FILING DATE: PCT Filing Date: 25-NOV-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.1340000/RWE  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6623 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: circular  
MOLECULE TYPE:  
US-08-244-434-36

Query Match 100.0%; Score 24; DB 2; Length 6623;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcctggttgacgct 24  
|||||

Db 6529 CAAGAATTCATGTTGACAGCT 6552

RESULT 6  
US-08-244-434-37  
Sequence 37, Application US/08244434  
Patent No. 5854004  
GENERAL INFORMATION:  
APPLICANT: Czeruliofsky, A.P.  
APPLICANT: Himmler, A.  
APPLICANT: Stralowa, C.  
APPLICANT: Weyer, U.  
APPLICANT: Lamche, H.  
APPLICANT: Sch fer, R.  
TITLE OF INVENTION: Process for Screening Substances Capable of  
TITLE OF INVENTION: Modulating a Receptor-Dependent Cellular Signal  
TITLE OF INVENTION: Transmission Path  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,434  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/92/02718  
FILING DATE: PCT Filing Date: 25-NOV-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ESMOND, ROBERT W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.1340000/RWE  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6630 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: circular  
US-08-244-434-37

Query Match 100.0%; Score 24; DB 2; Length 6630;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcattgttgacgct 24  
DB 6536 CACGAATTCATGTTGACAGCT 6559

RESULT 7  
US-08-125-462-2/c  
Sequence 2, Application US/08125462  
Patent No. 5840840  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,462  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-110-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6727 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..6727  
OTHER INFORMATION: /standard\_name="PET-11d-ANG-E6"  
US-08-125-462-2

Query Match 100.0%; Score 24; DB 2; Length 6727;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcattgttgacgct 24  
DB 1530 CACGAATTCATGTTGACAGCT 1507

RESULT 8  
US-08-891-848-2/c  
Sequence 2, Application US/08891848  
Patent No. 5955073  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,848  
FILING DATE: No. 5955073 yet assigned  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,462  
FILING DATE: 22-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,082  
FILING DATE: 04-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,195  
FILING DATE: 22-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/510,696  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-1103100S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6727 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..6727  
OTHER INFORMATION: /note="PET-11d-ANG-E6 fusion protein"  
OTHER INFORMATION: sequence"  
US-08-891-848-2

Query Match 100.0%; Score 24; DB 2; Length 6727;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaattcattgttgcagct 24  
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Db 1530 CAAGAATTCATGTTGCAGCT 1507

RESULT 9  
US-08-125-462-5/C  
Sequence 5, Application US/08125462  
Patent No. 5840840  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,462  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-110-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..6799  
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US-08-125-462-5  
Query Match 100.0%; Score 24; DB 2; Length 6799;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaattcattgttgcagct 24  
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Db 1602 CAAGAATTCATGTTGCAGCT 1579

RESULT 10  
US-08-891-848-5/C  
Sequence 5, Application US/08891848  
Patent No. 595073  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,848  
FILING DATE: No. 595073 yet assigned  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,462  
FILING DATE: 22-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,082  
FILING DATE: 04-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,195  
FILING DATE: 22-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/510,696  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-110310US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..6799  
OTHER INFORMATION: /note="PET-11d-E6-FB-EDN fusion protein sequence"  
US-08-891-848-5  
Query Match 100.0%; Score 24; DB 2; Length 6799;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 caagaattcattgttgcagct 24  
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Db 1602 CAAGAATTCATGTTGCAGCT 1579

Fri Dec 14 09:21:22 2001

us-09-631-709-5.rni

Page 6

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RESULT 11
PCT-US96-05611A-12
Sequence 12, Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Matlis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8540 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-3P Eukaryotic
PCT-US96-05611A-12
Query Match 100.0%; Score 24; DB 5; Length 8540;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 6105 CAAGAATTCATGTTTGACAGCT 6128
RESULT 12
PCT-US92-08258-6
Sequence 6, Application PC/TUS9208258
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC. and STATE OF OREGON BY AND
THROUGH THE OREGON STRAT
```

```

TITLE OF INVENTION: PRODUCTION OF GPA NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08258
FILING DATE: 19920929
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9861
TELEFAX: 415/952-9861
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8575 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-08258-6
Query Match 100.0%; Score 24; DB 5; Length 8575;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgacagct 24
Db 8541 CAAGAATTCATGTTTGACAGCT 8564
RESULT 13
US-08-252-493C-8
Sequence 8, Application US/08252493C
Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matlis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
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CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fidel, Seth A.  
REGISTRATION NUMBER: 38,449  
REFERENCE/DOCKET NUMBER: ALX-138  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 776-1790  
TELEFAX: (203) 772-3655  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8932 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Circular  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: Apex-3 Eukaryotic  
DESCRIPTION: Expression Vector  
US-08-252-493C-8

Query Match 100.0%; Score 24; DB 2; Length 8932;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgcagct 24  
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Db 6497 CAAGATTCATGTTGCAGCT 6520

## RESULT 14

US-09-276-197-8  
Sequence 8, Application US/09276197  
Patent No. 6040428  
GENERAL INFORMATION:  
APPLICANT: Rollins, Scott  
APPLICANT: Rother, Russell P.  
APPLICANT: Evans, Mark J.  
APPLICANT: Matlis, Louis A.  
TITLE OF INVENTION: PORCINE E-SELECTIN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seth A. Fidel  
STREET: 25 Science Park, Box 15  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06511  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 750 Kb storage  
COMPUTER: PC compatible  
OPERATING SYSTEM: DOS 6.2  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/276,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/252,493  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fidel, Seth A.  
REGISTRATION NUMBER: 38,449  
REFERENCE/DOCKET NUMBER: ALX-138  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 776-1790  
TELEFAX: (203) 772-3655  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8932 base pairs  
TYPE: Nucleic Acid

STRANDEDNESS: Double  
TOPOLOGY: Circular  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: Apex-3 Eukaryotic  
DESCRIPTION: Expression Vector  
US-09-276-197-8

Query Match 100.0%; Score 24; DB 3; Length 8932;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgcagct 24  
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Db 6497 CAAGATTCATGTTGCAGCT 6520

## RESULT 15

US-08-196-259-2  
Sequence 2, Application US/08196259  
Patent No. 5639596  
GENERAL INFORMATION:  
APPLICANT: BORNKAM, Georgy  
APPLICANT: POLACK, Axel  
TITLE OF INVENTION: DNA CONSTRUCT AND IN VITRO TEST FOR  
TITLE OF INVENTION: DETECTING TUMOR PROMOTERS BY MEANS OF SAID DNA CONSTRUCT  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENCER, FRANK & SCHNEIDER  
STREET: Suite 300 East - 1100 New York Ave., N.W.  
CITY: Washington  
STATE: DC

COUNTRY: US  
ZIP: 20005-3955

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/196,259  
FILING DATE: 25-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Spencer, George H.  
REGISTRATION NUMBER: 18,038  
REFERENCE/DOCKET NUMBER: FRK 0449  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 414-4000  
TELEFAX: (202) 414-4040

TELEX: 64267  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11616 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO PCT/DE91/00652  
FILING DATE: 16-AUG-1991  
PUBLICATION DATE: 04-MAR-1993

US-08-196-259-2

Query Match 100.0%; Score 24; DB 1; Length 11616;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgcagct 24  
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Fri Dec 14 09:21:22 2001

Db 11236 CAAGAATTCATCTTGACAGCT 11259

Search completed: December 13, 2001, 13:32:32  
Job time: 346 sec

us-09-631-709-5.rni



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:43:12 ; Search time 496.49 Seconds  
(Without alignments)  
41.443 Million cell updates/sec

Title: US-09-631-709-5

Perfect score: 24  
Sequence: 1 caagaattcattgtttacagact 24

Scoring table:  
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Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	24	100.0	24	AAH46618	Primer #5. Synthe
3	24	100.0	29	AAH46618	Plasmid pXc.1 PCR
4	24	100.0	35	AAH46618	Uridase expression
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6	24	100.0	3188	AAH46618	Sequence of plasmid
7	24	100.0	3276	AAH46618	Sequence of plasmid
8	24	100.0	3383	AAH46618	Sequence of plasmid
9	24	100.0	3427	AAH46618	Sequence of plasmid
10	24	100.0	3547	AAH46618	Plasmid sequence e
11	24	100.0	3557	AAH46618	Human pro-growth h

12	24	100.0	3621	7	AAH46618
13	24	100.0	3628	15	AAH46618
14	24	100.0	3854	17	AAH46618
15	24	100.0	3979	11	AAH46618
16	24	100.0	5552	21	AAH46618
17	24	100.0	6264	21	AAH46618
18	24	100.0	6354	21	AAH46618
19	24	100.0	6422	21	AAH46618
20	24	100.0	6623	14	AAH46618
21	24	100.0	6630	14	AAH46618
22	24	100.0	6652	21	AAH46618
23	24	100.0	6675	21	AAH46618
24	24	100.0	6727	20	AAH46618
25	24	100.0	6727	20	AAH46618
26	24	100.0	6799	20	AAH46618
27	24	100.0	6799	20	AAH46618
28	24	100.0	6961	21	AAH46618
29	24	100.0	7013	21	AAH46618
30	24	100.0	7114	21	AAH46618
31	24	100.0	8540	16	AAH46618
32	24	100.0	8540	17	AAH46618
33	24	100.0	8575	14	AAH46618
34	24	100.0	8932	20	AAH46618
35	24	100.0	8932	21	AAH46618
36	24	100.0	10332	20	AAH46618
37	24	100.0	10380	20	AAH46618
38	24	100.0	11265	19	AAH46618
39	24	100.0	11616	15	AAH46618
40	24	100.0	11616	15	AAH46618
41	24	100.0	16080	21	AAH46618
42	24	100.0	19798	22	AAH46618
43	24	100.0	19912	22	AAH46618
44	24	100.0	20160	22	AAH46618
45	24	100.0	20217	22	AAH46618

## ALIGNMENTS

RESULT 1	
ID	AAH46618 standard; DNA; 24 BP.
XX	
AC	AAH46618:
XX	
DF	17-SEP-2001 (first entry)
XX	
DE	Synthetic oligonucleotide #21.
XX	
KW	Helicobacter pylori; alpha-1,2-fucosyltransferase;
XX	fucose-containing sugar production; Lewis antigen; ss.
OS	Synthetic.
XX	
PN	MO200146400-AL.
XX	
PD	28-JUN-2001.
XX	
PF	20-DEC-2000; 2000WO-JP09033.
XX	
PR	21-DEC-1999; 99JP-0362243.
XX	
PA	(KYOW ) KYOWA HAKKO KOCYO KK.
XX	
PI	Endo T, Koizumi S, Tabata K, Ozaki A;
XX	
DR	WPI: 2001-418061/44.
XX	
PT	Modified alpha-1,2-fucosyltransferase gene and its expression product
PT	for efficient production of fucose-containing sugars such as Lewis
XX	antigen
PS	Example 3; Page 63; 69pp; Japanese.

Human pre-prolactin  
Plasmid sequence e  
Plasmid pSEC-cyt/c  
Sequence of plasmid  
pDIP/PyCSP.1 plasm  
Destination vector  
Destination vector  
Destination vector  
Sequence of circuli  
Sequence of circuli  
Destination vector  
Destination vector  
PET-11d-ANG-E6 DNA  
Nucleic acid sequ  
PET-11d-E6-FB-EDN  
Nucleic acid sequ  
Nucleic acid sequ  
Destination vector  
Destination vector  
Eukaryotic express  
Vector PAPEx-3p.  
Sequence of pHEB03  
Apex-3 eukaryotic  
Vector PAPEx-3. S  
Nucleotide sequenc  
Nucleotide sequenc  
Plasmid PREP7::CTL  
Vector PHEBO-DR-LU  
Construct PHEBO-DR  
DNA clone PCR C1.  
Nucleic acid sequ  
Nucleic acid sequ  
Nucleic acid sequ  
Nucleic acid sequ

XX The invention relates to DNA encoding a modified form of the  
CC alpha-1,2-fucosyltransferase of *Helicobacter pylori*. The  
CC polycytosine sequence, the AAAAAG sequence and/or the number of TAA  
CC repeats has been modified in the DNA sequence. The modified gene is  
CC useful in the production of large amounts of fucose-containing  
CC sugars, such as Lewis antigens for medicinal use. The present  
CC sequence is an oligonucleotide provided in the specification.  
XX  
SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 1 caagaattctcatgtttgacagct 24

## RESULT 2

AAF62506  
ID AAF62506 standard; DNA; 24 BP.  
AC AAF62506;  
XX  
DT 08-MAY-2001 (first entry)  
XX  
DE Primer #5.  
XX  
KW Guanosine 5'-diphosphofucose; GDP-fucose;  
KW Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDM; immunotherapy;  
KW cardiovascular; infection; ss.  
XX  
OS Synthetic.  
XX  
PN EPI076096-A1.  
XX  
PD 14-FEB-2001.  
XX  
PF 10-AUG-2000; 2000EP-0117167.  
XX  
PR 10-AUG-1999; 99JP-0225889.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;  
XX  
DR WPI: 2001-193203/20.  
XX  
XX  
XX Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a  
XX substrate of complex carbohydrates for immunotherapy comprises  
XX employing microorganisms that convert guanosine  
XX 5'-diphospho-4-keto-6-deoxymannose to GDP-fucose  
XX  
XX  
XX Example 2; Page 12; 19pp; English.  
XX  
XX The present invention relates to producing guanosine  
XX 5'-diphosphofucose (GDP-fucose) by employing an enzyme source  
XX that is a culture broth of microorganisms. GDP-fucose is useful  
XX as a synthetic substrate of complex carbohydrates that are useful  
XX e.g. for immunotherapy for protection against cardiovascular  
XX diseases, or infections by bacteria or viruses. Guanosine  
XX 5'-diphospho-4-keto-6-deoxymannose (GKDM) is useful as  
XX an intermediate for the production of GDP-fucose.  
XX  
XX  
XX Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 1 caagaattctcatgtttgacagct 24

## RESULT 3

AAF81198  
ID AAF81198 standard; DNA; 29 BP.  
AC AAF81198;  
XX  
DT 30-MAY-2001 (first entry)  
XX  
DE Plasmid pXC.1 PCR primer #1.  
XX  
XX Adenovirus; Ad; replication selective; tumour specific;  
KW early gene 1A; E1A; cancer; restenosis; intimal proliferative disease;  
KW primary pulmonary hypertension; cytosolic; hypotensive; vasotropic;  
KW gene therapy; vaccine; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200123004-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 02-OCT-2000; 2000WO-US27212.  
XX  
PR 30-SEP-1999; 99US-0157224.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Molnar-Kimber K, Toyozumi T;  
XX  
DR WPI: 2001-266112/27.  
XX  
XX  
XX Replication selective adenovirus mutant with improved selectivity for  
XX tumor and hyperproliferative cells, for use in treating cancer and  
XX hypertension, comprises a deactivated or crippled early gene promoter  
XX  
XX  
XX Example 1; Page 35; 56pp; English.  
XX  
XX The present sequence is a primer which was used in an example  
XX illustrating an invention relating to a replication selective adenovirus  
XX (Ad) mutant under the control of a tumour specific promoter. The Ad early  
XX gene 1A (E1A) promoter has been deactivated or crippled to reduce  
XX activity of the promoter to a lower level than wild-type Ad.  
XX The adenovirus is useful for delivering a heterologous gene or gene  
XX fragment, suicide gene or therapeutic gene, to a target cell. It is  
XX also useful for treating a patient suffering from cancer, carcinoma,  
XX diseases, neoplasm, leukemia, lymphoma or hyperproliferative cell  
XX diseases, including restenosis, intimal proliferative disease and  
XX primary pulmonary hypertension.  
XX  
XX  
XX Sequence 29 BP; 8 A; 6 C; 4 G; 11 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 4 caagaattctcatgtttgacagct 27

## RESULT 4

AAO40964  
ID AAO40964 standard; DNA; 35 BP.  
AC AAO40964;

```

XX 06-OCT-1993 (first entry)
DE Uracase expression plasmid construction PCR primer.
XX Enzyme; uric acid; oxidation; allantoin; hydrogen peroxide; CO2;
XX production; blood; urine; determination; hair dye; dyeing;
XX polymerase chain reaction; 5'end; ss.
OS Synthetic.
XX EP545688-A.
XX 09-JUN-1993.
XX 02-DEC-1992; 92EP-0311004.
XX 04-DEC-1991; 91JP-0320525.
XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX Azuma M, Hasegawa M, Hashimoto Y, Ishino S, Iwata K, Teshiba S;
XX Yagasaki M, Yamaguchi K, Yano K, Yokoo Y;
XX WPI; 1993-184382/23.
XX DNA encoding uricase and process for producing uricase - used in
XX determining uric acid content of blood or urine and in hair
XX dyeing kits, etc.
XX Example; Page 14; 22pp; English.
XX The sequence is that of a 5'-end PCR primer, which was used in the
XX construction of an efficient uricase expression plasmid. It was
XX used to change the SD sequence of vector pTRS3 into the SD sequence
XX of lacZ.
XX Sequence 35 BP; 9 A; 8 C; 5 G; 13 T; 0 other;
SQ
Query Match 100.0%; Score 24; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
Db 4 caagaattcattgttgcagct 27
RESULT 5
AAQ72263
ID AAQ72263 standard; DNA; 35 BP.
XX AAQ72263;
XX 09-JUN-1995 (first entry)
XX PCR primer for constructing lacZ-contg. plasmid pTL33.
XX Cellulomonas flavigena SK-4; uricase; catalase katG gene; Kate gene;
XX inactivation; catalase-deficient bacterium; tryptophan promoter;
XX recombinant oxidase production; beta-galactosidase; ss.
XX Synthetic.
XX JP06245762-A.
XX 06-SEP-1994.
XX 25-FEB-1993; 93JP-0036424.
XX 25-FEB-1993; 93JP-0036424.
XX

```

```

PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX WPI; 1994-321275/40.
XX Prepn. of oxidase - using catalase deficient Escherichia sp.
XX Example 1; Page 13; 15pp; Japanese.
XX PCR primers AAQ72263-Q72264 were used in the construction of the
XX plasmid pTL33 which contains a trip-lac fusion. Plasmid pTL33 was
XX used in the construction of pUT118 for expression of the uricase
XX gene from Cellulomonas flavigena SK-4, placed downstream of the
XX tryptophan promoter. A catalase-deficient strain of bacteria was
XX prepared by substituting the katG and Kate genes with katG::CAT
XX and Kate::KAM fusion genes. The catalase-deficient E.coli are then
XX used as hosts for recombinant production of uricase.
XX Sequence 35 BP; 9 A; 8 C; 5 G; 13 T; 0 other;
SQ
Query Match 100.0%; Score 24; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
Db 4 caagaattcattgttgcagct 27
RESULT 6
AAQ06310/C
ID AAQ06310 standard; DNA; 3188 BP.
XX AAQ06310;
XX 29-JAN-1991 (first entry)
XX Sequence of plasmid p79DBAM.
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX LTR 279..335
XX polyA_signal /*tag= a
XX /*tag= 497..502
XX /*tag= b
XX EP393502-A.
XX 24-OCT-1990.
XX 11-APR-1990; 90EP-0106992.
XX 19-APR-1989; 89EP-0810295.
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX Fountoulakis M, Garotta G, Stuber D;
XX WPI; 1990-322042/43.
XX Soluble interferon-gamma receptors - for treating auto-immune
XX diseases, chronic inflammations, etc.
XX Disclosure; Fig 49; 174pp; English.
XX IFN-gamma is a therapeutically active agent in the treatment
XX of autoimmune disease, allograft transplant rejections, multiple
XX sclerosis, chronic inflammations and delayed hypersensitivity. It is
XX also useful in identifying IFN-gamma agonists and antagonists.

```



```

XX Sequence of plasmid p267BGL.
DE
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
KM hypersensitivity; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT LRR 279..492
FT /*tag= a
FT CDS 493..585
FT /*tag= b
FT Sig-peptide 493..564
FT /*tag= c
FT polyA_signal /label= S.P.2
FT 736..741
FT /*tag= d
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990: 90EP-0106992.
XX
XX 19-APR-1989: 89EP-0810295.
XX
XX (HOF ) HOFFMANN-LA ROCHE AG.
XX
XX Fountoulakis M, Garotta G, Stuber D;
XX
XX WPI: 1990-322042/43.
XX
XX P-PSDB; AAR07067.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune
PT diseases, chronic inflammations, etc.
XX
XX Disclosure; Fig 59; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment
CC of autoimmune disease, allograft transplant rejections, multiple
CC sclerosis, chronic inflammations and delayed hypersensitivity. It is
CC also useful in identifying IFN-gamma agonists and antagonists.
CC See also AAQ06301.
XX
XX Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 11; Length 3427;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttcagcgt 24  
|||||  
Db 881 CAAGAATTCATGTTCACAGCT 858

RESULT 10  
AAN60846  
ID AAN60846 standard; DNA: 3547 BP.  
XX  
XX AAN60846;  
XX  
XX 24-OCT-1991 (first entry)  
XX  
XX Plasmid sequence encoding bovine pre-growth hormone.  
XX  
XX E.coli; pre-prolactin; bGH; bPRL; ds.  
XX  
XX Bos taurus.  
XX  
XX JP61202691-A.  
XX

```

PD 08-SEP-1986.
XX
XX 04-MAR-1985; 85JP-0042406.
XX
XX 04-MAR-1985; 85JP-0042406.
XX
XX (NAKA/) NAKAJIMA K.
XX
XX WPI: 1986-276389/42.
XX
XX Plasmid(s) contg. ampicillin resistant genes - for amplification
PT of bovine growth hormone and prolactin genes.
XX
XX Disclosure; Table 1-18; 13pp; Japanese.
XX
XX The bovine pre-growth hormone encoding sequence is derived from
CC pituitary tissue. The plasmids carry an amp resistance gene and,
CC and may be expressed by an E.coli host in an ampicillin medium
CC for efficient and large scale production of the hormone.
XX
XX Sequence 3547 BP; 901 A; 902 C; 912 G; 832 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 7; Length 3547;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttcagcgt 24  
|||||  
Db 3513 caagaattcattgttcagcgt 3536

RESULT 11  
AAN60801  
ID AAN60801 standard; DNA: 3557 BP.  
XX  
XX AAN60801;  
XX  
XX 24-OCT-1991 (first entry)  
XX  
XX Human pro-growth hormone.  
XX  
XX Pituitary gland; E.coli; ds.  
XX  
XX Homo sapiens.  
XX  
XX JP61202689-A.  
XX  
XX 08-SEP-1986.  
XX  
XX 04-MAR-1985; 85JP-0042404.  
XX  
XX 04-MAR-1985; 85JP-0042404.  
XX  
XX (NAKA/) NAKAJIMA K.  
XX  
XX WPI: 1986-276387/42.  
XX  
XX Plasmid for amplification of human growth hormone gene - derived
PT from human pituitary gland tissue.  
XX  
XX Disclosure; Table 1-9; 9pp; Japanese.  
XX  
XX Sequence is derived from human pituitary gland tissue, and allows
CC pro-growth hormone to be produced by a circular plasmid carrying an
CC amp resistance gene, from a transformed E.coli expression system in
CC an ampicillin containing medium.  
XX See also J61202690.  
XX  
XX Sequence 3557 BP; 927 A; 902 C; 897 G; 831 T; 0 other;  
SQ

Query Match 100.0%; Score 24; DB 7; Length 3557;

Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgacagct 24  
|||||  
Db 3523 caagaattcctcattgttgacagct 3546

## RESULT 12

AAN60847  
ID AAN60847 standard; DNA; 3621 BP.

AC AAN60847;

DT 24-OCT-1991 (first entry)

DE Human pre-prolactin gene.

KW Pituitary gland; E.coli; ds.

OS Homo sapiens.

PN JP61202690-A.

PD 08-SEP-1986.

PE 04-MAR-1985; 85JP-0042405.

PR 04-MAR-1985; 85JP-0042405.

PA (NAKA/) NAKAJIMA K.

DR WPI: 1986-276388/42.

PT Plasmid for amplification of the human prolactin gene - derived from human pituitary tissue and cultivated in ampicillin contg. medium to obtain a PBR 322 ampicillin resistant gene.

PS Disclosure; Table 1-9; 9pp; Japanese.

CC Sequence is derived from human pituitary gland tissue, and allows pre-prolactin to be produced by a circular plasmid carrying an amp resistance gene, from a transformed E.coli expression system in an ampicillin containing medium.

CC See also JP61202689.

Query Match 100.0%; Score 24; DB 7; Length 3621;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgacagct 24  
|||||  
Db 3587 caagaattcctcattgttgacagct 3610

## RESULT 13

AAN60848  
ID AAN60848 standard; DNA; 3628 BP.

AC AAN60848;

DT 24-OCT-1991 (first entry)

DE Plasmid sequence encoding bovine pre-prolactin hormone.

KW E.coli; growth hormone; bGH; bPRL; ds.

OS Bos taurus.

PN JP61202691-A.

XX 08-SEP-1986.

XX 04-MAR-1985; 85JP-0042406.

XX 04-MAR-1985; 85JP-0042406.

XX (NAKA/) NAKAJIMA K.

XX WPI: 1986-276389/42.

PT Plasmid(s) contg. ampicillin resistant genes - for amplification of bovine growth hormone and prolactin genes.

PS Disclosure; Table 1-18; 13pp; Japanese.

CC The bovine pre-prolactin hormone encoding sequence is derived from CC pituitary tissue. The plasmids carry an amp resistance gene and, CC and may be expressed by an E.coli host in an ampicillin medium CC for efficient and large scale production of the hormone.

CC Sequence 3628 BP; 965 A; 873 C; 901 G; 889 T; 0 other;

Query Match 100.0%; Score 24; DB 7; Length 3628;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgacagct 24  
|||||  
Db 3594 caagaattcctcattgttgacagct 3617

## RESULT 14

AA067221  
ID AA067221 standard; DNA; 3854 BP.

AC AA067221;

DT 24-MAR-1995 (first entry)

DE Plasmid pSEC-cyt/c DNA encoding pre-apo-protein.

KW Plasmid pSEC-cyt/c; vector; holo-protein; pre-apo-protein;

OS protein synthesis; Escherichia coli; cytoplasm cytochrome; ss.

XX Synthetic.

PH Key Location/Qualifiers

FT misc\_feature 396..454

FT promoter 2948..2962

FT misc\_feature 2996..3001

FT sig\_peptide 3009..3074

FT misc\_feature 3075..3374

FT misc\_feature 3375..3482

FT misc\_feature 3375..3482

FT misc\_feature 3375..3482

FT misc\_feature 3375..3482

PN WO9417191-A.

PD 04-AUG-1994.

PF 27-JAN-1994; 94WO-GB00161.

```

XX 27-JAN-1993; 93GB-0001553.
XX
XX (UYWA-) UNIV COLLEGE WALES.
XX
XX Kaderbhal MA;
XX
XX WPI: 1994-264104/32.
XX
XX P-PSDB; AAR57733.
XX
XX Genetic precursor unit causing periplasmic translocation of
XX pre-apo-protein - for processing the halo-protein, useful in
XX protein synthesis, assay of signal peptidase and identification
XX of its inhibitors
XX
XX Claim 10; Fig.5; 32pp; English.
XX
XX This plasmid contains a DNA sequence encoding the pre-form of an apo-
XX protein such that the pre-apo-protein is translocated from a
XX cytoplasmic cell region to a periplasmic region where formation of
XX process apo-protein and conversion to halo-protein to occur. The
XX DNA encoded in this plasmid is expressed in the cytoplasm of E. coli,
XX especially TB-1 and M830-1. The apo-protein is a cytoplasmic
XX cytochrome, especially having a soluble core domain of cytochrome-b5
XX of liver endoplasmic reticulum. The sequence also encodes an E.
XX coli alkaline phosphatase signal peptide.
XX
XX Sequence 3854 BP; 1005 A; 938 C; 965 G; 946 T; 0 other;
XX

```

```

Query Match 100.0%; Score 24; DB 15; Length 3854;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 caagaattctcatgtttgacagct 24
    |||||
Db 2689 caagaattctcatgtttgacagct 2712

```

```

RESULT 15
AAQ06312/C
ID AAQ06312 standard; DNA; 3979 BP.
XX
XX AAQ06312;
XX
XX 29-JAN-1991 (first entry)
XX
XX Sequence of plasmid p264BGL.
XX
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX LTR 279..242 /*tag= a
XX FT 243..426 /*tag= b
XX FT 243..405 /*tag= c
XX FT 1288..1292 /*tag= d
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990; 90EP-0106992.
XX
XX 19-APR-1989; 89EP-0810295.
XX

```

```

PA (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Fountoulakis M, Garotta G, Stuber D;
XX
XX WPI: 1990-322042/43.
XX
XX P-PSDB; AAR07066.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune
XX diseases, chronic inflammations, etc.
XX
XX Disclosure; Fig 55; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment
XX of autoimmune disease, allograft transplant rejections, multiple
XX sclerosis, chronic inflammations and delayed hypersensitivity. It is
XX also useful in identifying IFN-gamma agonists and antagonists.
XX See also AAQ06301.
XX
XX Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 other;
XX

```

```

Query Match 100.0%; Score 24; DB 11; Length 3979;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 caagaattctcatgtttgacagct 24
    |||||
Db 1433 CAAGAATTCTCATGTTTGACAGCT 1410

```

```

Search completed: December 13, 2001, 15:43:13
Job time: 8187 sec

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Fri Dec 14 09:21:22 2001

us-09-631-709-5.rng

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Page 8



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:35:42 ; Search time 1854.2 Seconds

(without alignments)  
213.533 Million cell updates/sec

Title: US-09-631-709-5

Sequence: 1 caagaattctcatgttgacagct 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_in:\*  
32: em\_htgo\_rod:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

8

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6 AX137661	AX137661 Sequence
2	24	100.0	35	6 E06705	E06705 PCR primer.
3	24	100.0	41	12 SYNS188V	K02384 Plasmid vec
4	24	100.0	43	12 SYNS2421	K02386 Plasmid vec
5	24	100.0	55	6 A31312	A31312 DNA fragmen
6	24	100.0	55	6 A31313	A31313 DNA fragmen
7	24	100.0	55	6 150064	150064 Sequence 1
8	24	100.0	62	1 E00952	E00952 Sequence 1
9	24	100.0	200	12 E00952	E00952 Plasmid pBR
10	24	100.0	1764	6 E08771	M10197 Plasmid pBR
11	24	100.0	1797	6 E08771	E08771 DNA encodin
12	24	100.0	103265	6 E01322	E01322 Sequence 4
13	24	100.0	2256	6 E08770	E01322 DNA transfe
14	24	100.0	3300	6 E00974	E08770 DNA encodin
15	24	100.0	3387	6 E00974	AE01974 Agrobacte
16	24	100.0	3468	6 E00954	E00974 cDNA encodi
17	24	100.0	3477	6 E00952	E00954 Plasmid for
18	24	100.0	3541	6 E00953	E00952 Plasmid DNA
19	24	100.0	3549	6 E00955	E00953 Plasmid for
20	24	100.0	3773	12 SYNPT551V	E00955 Plasmid for
21	24	100.0	3809	12 SYNPT511V	L09154 pMT511 expr
22	24	100.0	3918	6 AR077142	L09153 pMT511 expr
23	24	100.0	4151	1 RCFDXE	AR077142 Sequence
24	24	100.0	4753	1 BTN6407	Y11304 R. capsulatu
25	24	100.0	4892	12 XXU02429	AJ006407 Bacillus
26	24	100.0	4896	12 XXU13868	U02429 Cloning vec
27	24	100.0	4985	12 AF147464	U13868 pSVL clonin
28	24	100.0	5066	12 SCU40398	AF147464 T7 expres
29	24	100.0	5228	12 XXU25059	U40398 Synthetic c
30	24	100.0	5345	12 SYNPT288V	U25059 Cloning vec
31	24	100.0	5347	12 SYNPT289V	L09147 PUR289 clon
32	24	100.0	5348	12 SYNPT291V	L09148 PUR289 clon
33	24	100.0	5349	12 SYNPT292V	L09150 PUR291 clon
34	24	100.0	5351	12 SYNPT292V	L09151 PUR292 clon
35	24	100.0	5353	12 SYNPT290V	L09146 PUR278 clon
36	24	100.0	6433	12 AF020539	L09149 PUR290 clon
37	24	100.0	6623	6 AR068550	AF020539 Shuttle v
38	24	100.0	6630	6 A23373	AR068550 Sequence
39	24	100.0	6630	6 AR068551	A23373 Artificial
40	24	100.0	6727	6 AR060673	AR068551 Sequence
41	24	100.0	6727	6 AR074430	AR060673 Sequence
42	24	100.0	6799	6 AR060676	AR074430 Sequence
43	24	100.0	6799	6 AR074433	AR060676 Sequence
44	24	100.0	8097	12 SCU46780	AR074433 Sequence
45	24	100.0	8932	6 AR069417	U46780 Synthetic c

## ALIGNMENTS

RESULT 1  
AX137661  
LOCUS AX137661  
DEFINITION Sequence 5 from Patent EP1076096.  
ACCESSION AX137661  
VERSION AX137661.1 GI:14273846  
KEYWORDS  
ORGANISM  
SOURCE  
synthetic construct.  
synthetic construct  
artificial sequence.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Koizumi,S., Nagano,H., Endo,T., Tabata,K. and Ozaki,A.  
TITLE Process for producing gdp-fucose  
JOURNAL Patent: EP 1076096-A 5 14-FEB-2001;  
KYOWA HAKKO KOGYO CO., LTD. (JP)

FEATURES  
Source  
1..24  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Synthetic DNA"

BASE COUNT 7 a 5 c 4 g 8 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
DB 1 CAAGAATTCATCATGTTTGACAGCT 24

## RESULT 2

LOCUS E06705 35 bp DNA PAT 29-SEP-1997  
DEFINITION PCR primer.  
ACCESSION E06705 1 GI:2174867  
VERSION JP 1994038766-A/7.  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequence.

## REFERENCE

1 (bases 1 to 35)

## AUTHORS

Iagasaki,M., Ishino,S., Iwata,K., Azuma,M., Teshiba,S.,  
Hasegawa,M., Yamaguchi,K., Yano,K., Yokoo,Y. and Hashimoto,Y.  
URICASE GENE AND PRODUCTION OF URICASE  
Patent: JP 1994038766-A 7 15-FEB-1994;

## JOURNAL

KYOWA HAKKO KOGYO CO LTD

## COMMENT

OC Artificial gene  
PN JP 1994038766-A/7  
PD 15-FEB-1994  
PE 04-DEC-1991 JP 1991320525

PI YAGASAKI MAKOTO, ISHINO SHUICHI, IWATA KAZUHISA, PI AZUMA  
MASAYUKI,

PI TESHIBA SADAQ, HASEGAWA MASARU, YAMAGUCHI KAZUO, YANO KEIICHI,  
PI YOKOO YOSHIMARU, HASHIMOTO YUKIO

PC C12N15/53, C12N1/20, C12N1/21, C12N9/06, (C12N15/53, C12R1:01), PC  
(C12N1/20,

PC C12R1:01), (C12N1/21, C12R1:19), (C12N9/06, C12R1:19), (C12N9/06,  
PC C12R1:01);

CC strandedness: Single;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

## FEATURES

location/Qualifiers

## source

1..35  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 9 a 8 c 5 g 13 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
DB 4 CAAGAATTCATCATGTTTGACAGCT 27

## RESULT 3

LOCUS SYNS188V 41 bp DNA SYN 27-APR-1993  
DEFINITION Plasmid vector pBR3188 derived from deletion of 12 bp of pBR322,  
destroying Tc-promoter.  
ACCESSION K02384  
VERSION K02384.1 GI:2093117  
KEYWORDS drug resistance protein; mutational analysis; promoter region;  
tetracycline resistance.  
SOURCE pBR322 DNA, clone pBR 188.

## ORGANISM

unidentified cloning vector

artificial sequence; vectors.

## REFERENCE

1 (bases 1 to 41)

## AUTHORS

Savochkina,L.P., Retchinsky,V.O. and Beabealashvili,R.S.

Stability of cloned promoter-containing fragments

## JOURNAL

Mol. Gen. Genet. 189, 142-147 (1983)

## MEDLINE

83218507

## COMMENT

[1] inserted strong promoters from T7 and lambda into pBR322  
derived promoter-probe vectors. The inserted promoters, which  
occurred in dissimilar environments, served as promoters for the  
pBR322 tetracycline resistance operon. Promoter strength was  
measured by Tc resistance. Plasmids containing T7 A2 promoters  
appeared to confer less Tc resistance than those containing A3  
promoters.

## FEATURES

location/Qualifiers

## source

1..41  
/organism="unidentified cloning vector"  
/db\_xref="taxon:45196"

BASE COUNT 9 a 10 c 8 g 14 t  
ORIGIN 10 bp upstream of EcoRI site.

## Query Match

100.0%; Score 24; DB 12; Length 41;

## Best Local Similarity

100.0%; Pred. No. 0.29;

## Matches

24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

1 caagaattctcatgtttgacagct 24

## DB

7 CAAGAATTCATCATGTTTGACAGCT 30

## RESULT 4

LOCUS SYNS2421 43 bp DNA SYN 27-APR-1993  
DEFINITION Plasmid vector pBR3242 derived from insertion of lac UV5 promoter-  
operator region into pBR322; region 5' to UV5 insertion.  
ACCESSION K02386  
VERSION K02386.1 GI:2093120  
KEYWORDS drug resistance protein; mutational analysis; promoter region;  
tetracycline resistance.

## SEGMENT

1 of 2

pBR322 DNA, clone pBR 242.

## SOURCE

synthetic construct

## ORGANISM

artificial sequence.

## REFERENCE

1 (bases 1 to 43)

## AUTHORS

Savochkina,L.P., Retchinsky,V.O. and Beabealashvili,R.S.

## TITLE

Stability of cloned promoter-containing fragments

## JOURNAL

Mol. Gen. Genet. 189, 142-147 (1983)

## MEDLINE

83218507

## COMMENT

[1] inserted strong promoters from T7 and lambda into pBR322  
derived promoter-probe vectors. The inserted promoters, which  
occurred in dissimilar environments, served as promoters for the  
pBR322 tetracycline resistance operon. Promoter strength was  
measured by Tc resistance. Plasmids containing T7 A2 promoters  
appeared to confer less Tc resistance than those containing A3  
promoters.

## FEATURES

location/Qualifiers

## source

1..43  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 11 a 10 c 6 g 16 t  
ORIGIN 10 bp upstream of EcoRI site.

Query Match 100.0%; Score 24; DB 12; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24

DB 7 CAAGAATTCATCATGTTTGACAGCT 30

RESULT 5  
LOCUS A31312 55 bp DNA PAT 03-NOV-1995  
DEFINITION DNA fragment (pBR322 restriction fragment) from patent WO9012321.  
ACCESSION A31312  
VERSION A31312.1 GI:1249336  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial construct.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS  
TITLE HALOGENATED DNA LIGAND RADIOSENSITISERS FOR CANCER THERAPY  
JOURNAL Patent: WO 9012321-A 1 18-OCT-1990;  
FEATURES Location/Qualifiers  
source 1..55  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 13 a 13 c 10 g 19 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 17 CAAGAATTCTCATGTTTGACAGCT 40

RESULT 6  
LOCUS A31313 55 bp DNA PAT 03-NOV-1995  
DEFINITION DNA fragment (pBR322 restriction fragment) from patent WO9012321.  
ACCESSION A31313  
VERSION A31313.1 GI:1247258  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS  
TITLE HALOGENATED DNA LIGAND RADIOSENSITISERS FOR CANCER THERAPY  
JOURNAL Patent: WO 9012321-A 2 18-OCT-1990;  
FEATURES Location/Qualifiers  
source 1..55  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 19 a 10 c 13 g 13 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 39 CAAGAATTCTCATGTTTGACAGCT 16

RESULT 7  
LOCUS 150064 55 bp DNA PAT 07-OCT-1997  
DEFINITION Sequence 1 from patent US 5641764.  
ACCESSION 150064  
VERSION 150064.1 GI:2472284  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 55)  
TITLE

AUTHORS Martin, R. Francis and Kelly, D. Patterson.  
TITLE Halogenated DNA ligand radiosensitizers for cancer therapy  
JOURNAL Patent: US 5641764 A 1 24-JUN-1997;  
FEATURES Location/Qualifiers  
source 1..55  
/organism="unknown"  
BASE COUNT 13 a 13 c 10 g 19 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 17 CAAGAATTCTCATGTTTGACAGCT 40

RESULT 8  
LOCUS ECOTEMPPO 62 bp DNA BCT 26-APR-1993  
DEFINITION E. coli tet promoter region.  
ACCESSION K01791  
VERSION K01791.1 GI:147933  
KEYWORDS mutational analysis; promoter region.  
SOURCE E. coli DNA.  
ORGANISM Escherichia coli  
REFERENCE 1 (bases 1 to 62)  
AUTHORS Russell, D. R. and Bennett, G. N.  
TITLE Construction and analysis of in vivo activity of E. coli promoter  
JOURNAL hybrids and promoter mutants that alter the -35 to -10 spacing  
MEDLINE Gene 20, 231-243 (1982)  
COMMENT [1] examines the efficiency of gene expression in E. coli if the distance between the -35 and -10 regions is changed. When two bases are inserted increasing the span to 19 there is no gene expression and when 1 base is inserted (as in tet 18 bp), expression is reduced to 50% of normal.  
FEATURES Location/Qualifiers  
source 1..62  
/organism="Escherichia coli"  
/db\_xref="taxon:562"  
-35-signal 20..25  
-10-signal 43..48  
BASE COUNT 17 a 11 c 10 g 24 t  
ORIGIN 41 bp upstream of HindIII site.

Query Match 100.0%; Score 24; DB 1; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24  
Db 5 CAAGAATTCTCATGTTTGACAGCT 28

RESULT 9  
LOCUS SYN313FR/C 200 bp DNA SYN 09-APR-1996  
DEFINITION Plasmid pBR313 DNA fragment.  
ACCESSION M10197 M28278  
VERSION M10197.1 GI:207771  
KEYWORDS  
SOURCE Cloning vector (sub-species Cloning vector pBR313) DNA.  
ORGANISM unidentified cloning vector  
REFERENCE 1 (bases 1 to 200)  
AUTHORS Wilkins, R. J.  
TITLE Selective binding of actinomycin D and distamycin A to DNA

JOURNAL Nucleic Acids Res. 10 (22), 7273-7282 (1982)  
MEDLINE 83116954  
FEATURES Location/Qualifiers  
source 1..200  
/organism="unidentified cloning vector"  
/sub\_species="Cloning vector pBR3.13"  
/db\_xref="taxon:45196"

BASE COUNT 58 a 33 c 43 g 66 t  
ORIGIN 31 bp upstream of EcoRI site.

Query Match 100.0%; Score 24; DB 12; Length 200;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcatgtttgacagct 24  
DB 39 CAAGAATTCATGTTGACAGCT 16

RESULT 10  
LOCUS E08771 1764 bp DNA PAT 29-SEP-1997  
DEFINITION DNA encoding hybrid protein of beta-glucuronidase and protein A.  
ACCESSION E08771  
VERSION E08771.1 GI:2176883  
KEYWORDS JP 1995051086-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1764)  
AUTHORS Jiyon,E.P. and Argusiu,A.  
TITLE HYBRID PROTEIN PRODUCED BY ULTRA-HIGH DEGREE PROCARYOTE EXPRESSION SYSTEM  
JOURNAL Patent: JP 1995051086-A 2 28-FEB-1995;  
REPLIGEN CORP

COMMENT OS None  
OC Artificial sequences.  
PN JP 1995051086-A/2  
PD 28-FEB-1995  
PF 07-MAR-1986 JP 1994069101  
PI JIYON ERU PAMMA, ARGUSIU ANIRTONISU  
PC C12P21/02.C07K19/00,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),  
PC C12R1:19;  
CC strandedness: Double;  
CC topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..1764  
FT FT /clone="pgb5" /organism="Artificial sequences" FT  
FT mac\_peptide 502..1764  
FT FT /product="Protein A-like hybrid protein".

FEATURES Location/Qualifiers  
source 1..1764  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 639 a 373 c 337 g 415 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 1764;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcatgtttgacagct 24  
DB 1747 CAAGAATTCATGTTGACAGCT 1724

RESULT 11  
I03265/c

LOCUS I03265 1797 bp ss-DNA PAT 21-MAY-1993  
DEFINITION Sequence 4 from Patent US 488280.  
ACCESSION I03265  
VERSION I03265.1 GI:270747  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1797)  
AUTHORS Palmer,J.L. and Anilionis,A.  
TITLE Hybrid proteins produced by an ultrahigh prokaryotic expression  
JOURNAL Patent: US 488280-A 4 19-DEC-1989;  
Repligen Corporation;  
Cambridge, MA

Query Match 100.0%; Score 24; DB 6; Length 1797;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcatgtttgacagct 24  
DB 1777 CAAGAATTCATGTTGACAGCT 1754

RESULT 12  
LOCUS E01322 2256 bp DNA PAT 29-SEP-1997  
DEFINITION DNA transfer vector encoding hybrid protein.  
ACCESSION E01322  
VERSION E01322.1 GI:2169581  
KEYWORDS JP 1987207297-A/1.  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 2256)  
AUTHORS Jiyon,E.P. and Argusiu,A.  
TITLE HYBRID PROTEIN PREPARED BY ULTRAHIGH PROCARYOTIC EXPRESSION SYSTEM  
JOURNAL Patent: JP 1987207297-A 1 11-SEP-1987;  
REPLIGEN CORP

COMMENT OS Artificial gene  
OC Artificial sequence; Genes.  
PN JP 1987207297-A/1  
PD 11-SEP-1987  
PF 07-MAR-1986 JP 1986048770  
PI JIYON ERU PAMMA, ARGUSIU ANIRTONISU  
PC C07K13/00,A61K35/74,A61K37/00,C07H21/04,C12N1/20,C12N15/00, PC  
C12P21/02  
PC (C12P21/02,C12R1:19);  
CC strandedness: Double;  
CC topology: Linear;  
CC hypothetical: NO;  
CC anti\_sense: NO;  
FH Key Location/Qualifiers  
FT misc-feature 1..2256  
FT FT /note="DNA transfer vector which encodes FT  
FT hybrid protein of  
FT beta-glucuronidase and A2 protein".

FEATURES Location/Qualifiers  
source 1..2256  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 767 a 478 c 474 g 537 t  
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2256;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttgacagct 24  
 ||||||||||||||||||||  
 Db 2239 CAAGAATTCATGTTTGACAGCT 2216

RESULT 13  
 E08770/c 2256 bp DNA PAT 29-SEP-1997  
 LOCUS DNA encoding hybrid protein of beta-glucuronidase and protein A.  
 DEFINITION E08770  
 ACCESSION E08770  
 VERSION E08770.1 GI:2176882  
 KEYWORDS JP 1995051086-A/1.  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 2256)  
 AUTHORS Jiyon, E.P. and Arugisu, A.  
 TITLE HYBRID PROTEIN PRODUCED BY ULTRA-HIGH DEGREE PROCARYOTE EXPRESSION SYSTEM  
 JOURNAL Patent: JP 1995051086-A 1 28-FEB-1995;  
 REPLICEN CORP  
 OS None  
 OC Artificial sequences.  
 PN JP 1995051086-A/1  
 PD 28-FEB-1995  
 PF 07-MAR-1986 JP 1994069101  
 PI JIYON ERU PAMAMA, ARUGISU ANIRIONISU  
 PC C12P21/02,C07K19/00,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),  
 PC (C12N1/21,  
 CC C12R1:19);  
 CC strandedness: Double;  
 CC topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1.2256  
 FT /organism='Artificial sequences' FT  
 FT /clone='pBg9', 502..2256  
 FT mat\_peptide /product='Protein A-like hybrid protein'.  
 FEATURES  
 source Location/Qualifiers  
 1..2256  
 /organism='unidentified'  
 /db\_xref='taxon:32644'  
 BASE COUNT 767 a 478 c 474 g 537 t  
 ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2256;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttgacagct 24  
 ||||||||||||||||||||  
 Db 2239 CAAGAATTCATGTTTGACAGCT 2216

RESULT 14  
 AF019744/c 3300 bp DNA BCT 02-APR-1998  
 LOCUS Agrobacterium tumefaciens plasmid pGV 3850:1003 T-DNA, left border.  
 DEFINITION Agrobacterium tumefaciens  
 ACCESSION AF019744  
 VERSION AF019744.1 GI:3004665  
 KEYWORDS  
 SOURCE Agrobacterium tumefaciens.  
 ORGANISM Agrobacterium tumefaciens  
 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 Rhizobiaceae; Rhizobium.  
 REFERENCE 1 (bases 1 to 3300)  
 AUTHORS Feldmann, K.A.

TITLE T-DNA insertion mutagenesis in Arabidopsis: seed  
 infection/transformation  
 JOURNAL Methods in Arabidopsis Research 10, 274-289 (1992)  
 REFERENCE 2 (bases 1 to 3300)  
 AUTHORS Tisler, C.P., Zambryski, P. and Feldmann, K.A.  
 TITLE Complete 3 kb left border sequence of the 3850:1003 T-DNA  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 3300)  
 AUTHORS Tisler, C.P., Zambryski, P. and Feldmann, K.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-AUG-1997) Plant Sciences, University of Arizona,  
 Forbes Building 303, Tucson, AZ 85721, USA  
 FEATURES  
 source Location/Qualifiers  
 1..3300  
 /organism='Agrobacterium tumefaciens'  
 /strain='C58 C1 R1f'  
 /db\_xref='taxon:358'  
 /plasmid='pGV 3850:1003'  
 misc\_feature 1..3300  
 /note='T-DNA left border'  
 BASE COUNT 901 a 679 c 769 g 932 t 19 others  
 ORIGIN

Query Match 100.0%; Score 24; DB 1; Length 3300;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttgacagct 24  
 ||||||||||||||||||||  
 Db 3052 CAAGAATTCATGTTTGACAGCT 3029

RESULT 15  
 E00974 3387 bp RNA PAT 29-SEP-1997  
 LOCUS cDNA encoding human growth factor 20K.  
 DEFINITION E00974  
 ACCESSION E00974  
 VERSION E00974.1 GI:2169235  
 KEYWORDS JP 1986224988-A/1.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3387)  
 AUTHORS Nakajima, K. and Nagai, J.  
 TITLE RECOMBINANT PLASMID OF ESCHERICHIA COLI FOR AMPLIFYING  
 JOURNAL COMPLEMENTARY DNA OF HUMAN GROWTH HORMONE 20K  
 Patent: JP 1986224988-A 1 06-OCT-1986;  
 NAKAJIMA KUNIO  
 COMMENT  
 OS Human  
 PN JP 1986224988-A/1  
 PD 06-OCT-1986  
 PF 29-MAR-1985 JP 1985066208  
 PI NAKAJIMA KUNIO, NAGAI JUN  
 PC C12N15/00//C12P21/02,(C12N15/00,C12R1:19);  
 CC strandedness: Double;  
 CC topology: Linear;  
 CC hypothetical: No;  
 CC anti-sense: No;  
 CC \*source: tissue=Intestine;  
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 source Location/Qualifiers  
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 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Dec 14 09:21:21 2001

us-09-631-709-5.rge

Page 6

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Db 3353 CAAGAATTCTCATGTTCACAGCT 3376

Search completed: December 13, 2001, 15:35:43  
Job time: 7737 Sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:03:33 ; Search time 5599.23 Seconds  
(without alignments)  
38.383 Million cell updates/sec

Title: US-09-631-709-2  
Perfect score: 20  
Sequence: 1 gactgactggttcgaagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estda:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: qd\_est1:\*  
11: qd\_est2:\*  
12: qd\_hic:\*  
13: qd\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_hiv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rtd:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	184	11	BG874396
2	20	100.0	185	11	BG874387
3	20	100.0	186	11	BG874391
4	20	100.0	194	11	BG874395
5	20	100.0	201	11	BG874379
6	20	100.0	202	11	BG874517
7	20	100.0	203	11	BG874381
8	20	100.0	203	11	BG874511
9	20	100.0	205	11	BG874394
10	20	100.0	206	10	AW994158
11	20	100.0	219	11	BG874516
12	20	100.0	220	11	BG874514

13	20	100.0	221	11	BG874513	BG874513	QV4-BN003
14	20	100.0	221	11	BG878325	BG878325	QV2-ST029
15	20	100.0	258	10	AV036275	AV036275	AV036275
16	20	100.0	349	11	BG063262	BG063262	H3005A05-
17	20	100.0	378	11	BG874522	BG874522	QV4-BN003
18	20	100.0	390	10	AA966183	AA966183	V4a04a1.f
19	20	100.0	469	13	AO640463	AO640463	927P1-13C
20	20	100.0	486	10	AA111347	AA111347	mo53f05.r
21	20	100.0	491	13	P859R	P859R	AL390539
22	20	100.0	507	10	AL499935	AL499935	AL499935
23	20	100.0	519	10	AM539899	AM539899	CO125H03-
24	20	100.0	588	13	A2124374	A2124374	SB122-t7
25	20	100.0	612	10	AL499952	AL499952	AL499952
26	20	100.0	699	10	AL500397	AL500397	AL500397
27	20	100.0	699	10	AL500414	AL500414	AL500414
28	20	100.0	703	10	AL500060	AL500060	AL500060
29	20	100.0	703	13	AG012834	AG012834	Homo sapi
30	20	100.0	705	13	AG012835	AG012835	Homo sapi
31	20	100.0	713	13	AG012836	AG012836	Homo sapi
32	20	100.0	720	13	AG000789	AG000789	Homo sapi
33	20	100.0	722	13	AG000790	AG000790	Homo sapi
34	20	100.0	723	13	AG000764	AG000764	Homo sapi
35	20	100.0	723	13	AG000765	AG000765	Homo sapi
36	20	100.0	1716	12	AK005545	AK005545	Mus muscu
37	20	100.0	1958	12	AK005492	AK005492	Mus muscu
38	18.4	92.0	367	11	BI285916	BI285916	UI-R-CX0S
39	18.4	92.0	387	10	AW491025	AW491025	UI-R-BH3-
40	18.4	92.0	437	10	AA490684	AA490684	UI-M-BH3-
41	18.4	92.0	660	11	BI285964	BI285964	UI-R-CX0S
42	18.4	92.0	759	11	BI285886	BI285886	UI-R-CX0S
43	18.4	92.0	763	11	BI284457	BI284457	UI-R-CX0S
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## ALIGNMENTS

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BG874396	BG874396	QV4-BN0025-010200-097-f12 BN0025	184 bp	mRNA	Homo sapiens	human.	
BG874396.1	GI:14251327	QV4-BN0025-010200-097-f12 BN0025	184 bp	mRNA	Homo sapiens	human.	
REFERENCE	AUTHORS	DIAS NETO, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H., Brunshtein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.					
TITLE	JOURNAL MEDLINE COMMENT	Shotgun Sequencing of the human transcriptome with ORF expressed sequence tags					
		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)					
		Contact: Simpson A.J.G.					
		Laboratory of Cancer Genetics					
		Ludwig Institute for Cancer Research					
		Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil					
		Tel: +55-11-2704922					
		Fax: +55-11-2707001					
		Email: asimpson@ludwig.org.br					
		This sequence was derived from the RAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL					
		(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV4-BN0025-010200-097-f12et3=2000-02-01et4=1)					
		Seq primer: puc 18 forward					

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High quality sequence stop: 184.

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/dev\_stage="Adult"

/note="Organ: breast:normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

# BASE COUNT

43 a 55 c 54 g 32 t

# ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 184;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20  
|||||  
Db 127 GAGCTGACTGGTTGAAGC 146

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LOCUS BG874387 185 bp mRNA EST 30-MAY-2001  
DEFINITION QV4-BN0025-010200-097-c12 BN0025 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG874387  
VERSION BG874387.1 GI:14251318  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 185)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# REFERENCE

1 (bases 1 to 185)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# JOURNAL MEDLINE COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV4-BN0025-010  
200-097-c12&t3=2000-02-01&t4=1)  
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# FEATURES

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/db\_xref="taxon:9606"  
/clone\_lib="BN0025"  
/dev\_stage="Adult"

/note="Organ: breast:normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

# BASE COUNT

43 a 55 c 54 g 32 t

# ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 184;

derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 41 a 58 c 54 g 32 t

# ORIGIN

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Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20  
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Db 128 GAGCTGACTGGTTGAAGC 147

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LOCUS BG874391 186 bp mRNA EST 30-MAY-2001  
DEFINITION QV4-BN0025-010200-097-e07 BN0025 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG874391  
VERSION BG874391.1 GI:14251322  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 186)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# REFERENCE

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV4-BN0025-010  
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/db\_xref="taxon:9606"  
/clone\_lib="BN0025"  
/dev\_stage="Adult"

# TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# JOURNAL MEDLINE COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV4-BN0025-010  
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Seq primer: puc 18 forward  
High quality sequence start: 16  
High quality sequence stop: 186.  
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/dev\_stage="Adult"

# FEATURES

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/note="Organ: breast:normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 43 a 55 c 54 g 34 t

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Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 129 GAGCTGACTGGTTGAAGC 148

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BG874395

LOCUS BG874395 194 bp mRNA EST 30-MAY-2001

DEFINITION QV4-BN0025-010200-097-f10 BN0025 Homo sapiens cDNA, mRNA sequence.

BG874395

ACCESSION BG874395.1 GI:14251326

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-QV4-BN0025-010200-097-f10&t3=2000-02-01&t4=1)  
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ORIGIN

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BG874379/c

LOCUS BG874379 201 bp mRNA EST 30-MAY-2001

DEFINITION QV4-BN0025-010200-097-a03 BN0025 Homo sapiens cDNA, mRNA sequence.

BG874379

ACCESSION BG874379.1 GI:14251310

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

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JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-QV4-BN0025-010200-097-a03&t3=2000-02-01&t4=1)  
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High quality sequence start: 20  
High quality sequence stop: 201.  
Location/Qualifiers

FEATURES

source

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Query Match 100.0%; Score 20; DB 11; Length 201;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctactggttggaagc 20  
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Db 39 GAGCTGACTGGTTGAAGC 20

## RESULT 6

BG874517

LOCUS BG874517 202 bp mRNA EST 30-MAY-2001

DEFINITION QV4-BN0036-140200-104-d03 BN0036 Homo sapiens cDNA, mRNA sequence.

BG874517

ACCESSION BG874517.1 GI:14251448

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 202)

## AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

## JOURNAL MEDLINE COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## FEATURES SOURCE

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QVA-BN0036-140  
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BASE COUNT 46 a 60 c 58 g 38 t  
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Query Match 100.0%; Score 20; DB 11; Length 202;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20  
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Db 145 GAGCTGACTGGGTGAAGC 164

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LOCUS BG874381 203 bp mRNA EST 30-MAY-2001

DEFINITION QV4-BN0025-010200-097-a10 BN0025 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG874381

VERSION BG874381.1 GI:14251312

## KEYWORDS

## SOURCE

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

## JOURNAL MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QVA-BN0025-010  
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/note="Organ: breast-normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 32 a 60 c 61 g 50 t  
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Best Local Similarity 100.0%; Pred. No. 40;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 42 GAGCTGACTGGGTGAAGC 23

## RESULT 8

LOCUS BG874511 203 bp mRNA EST 30-MAY-2001

DEFINITION QV4-BN0036-140200-104-a12 BN0036 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG874511

VERSION BG874511.1 GI:14251442

## KEYWORDS

## SOURCE

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

## JOURNAL MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Project. This entry can be seen in the following URL

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OY 1 gagctgactggttggaagc 20  
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 DB 149 GAGCTGACTGGTTGAAGCC 168

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 ACCESSION BG874516  
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 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 219)  
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 CONTACT: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4-BN0036-140  
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 Site:2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 52 a 67 c 63 g 37 t  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactggttggaagc 20  
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 DB 162 GAGCTGACTGGTTGAAGCC 181

RESULT 12  
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 DEFINITION OY4-BN0036-140200-104-c02 BN0036 Homo sapiens CDNA, mRNA sequence.  
 ACCESSION BG874514  
 VERSION BG874514.1 GI:14251445  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 220)  
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 CONTACT: Simpson A.J.G.  
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 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4-BN0036-140  
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 /note="Organ: breast,normal; Vector: puc18; Site:1: SmaI;  
 Site:2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
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OY 1 gagctgactggttggaagc 20  
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 ACCESSION BG874513  
 VERSION BG874513.1 GI:14251444  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1  
AUTHORS  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 221)  
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shogun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-QV4-BN0036-140  
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BASE COUNT  
52 a 68 c 63 g 38 t  
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Query Match 100.0%; Score 20; DB 11; Length 221;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 164 GAGCTGACTGCGTTGAAGC 183

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DEFINITION QV2-ST0298-240200-063-g01 ST0298 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BG878325  
VERSION BG878325.1 GI:14255415  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 221)  
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shogun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL  
MEDLINE  
COMMENT  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-QV2-ST0298-240  
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53 a 68 c 62 g 38 t  
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Qy 1 gaagctgactggtgaagc 20  
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Db 164 GAGCTGACTGCGTTGAAGC 183

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DEFINITION AV036275 Mus musculus adult C57BL/6J placenta Mus musculus cDNA  
ACCESSION AV036275  
VERSION AV036275.1 GI:4855940  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 258)  
Carninci, P., Shibata, K., Ozawa, Y., Kono, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuna, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomioka, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
RIKEN Mouse ESTs  
Unpublished (1999)  
Contact: Chie Owa  
Genome Science Laboratory  
RIKEN  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-9145  
Fax: 81-298-36-9098  
Email: genome-res@r.riken.go.jp  
Thermostabilization and thermoinactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA  
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

# FEATURES

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Job time: 5809 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 19:14:03 : Search time 2658.89 Seconds  
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Title: US-09-631-709-2

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Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 959380 seqs, 71176033 residues

Total number of hits satisfying chosen parameters: 1918760

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 3	20	100.0	5438	US-09-689-916-25	Sequence 25, Appl
C 4	20	100.0	5495	US-09-891-685A-4	Sequence 4, Appl
C 5	20	100.0	5556	US-09-891-685A-2	Sequence 2, Appl
C 6	20	100.0	5658	US-09-689-913-10	Sequence 10, Appl
C 7	20	100.0	5658	US-09-689-916-10	Sequence 10, Appl
C 8	20	100.0	5822	US-09-891-685A-8	Sequence 10, Appl
C 9	20	100.0	6046	US-09-891-685A-15	Sequence 15, Appl
C 10	20	100.0	6166	US-09-611-451-51	Sequence 51, Appl
C 11	20	100.0	6269	US-09-891-685A-9	Sequence 9, Appl
C 12	20	100.0	6299	US-09-891-685A-10	Sequence 10, Appl
C 13	20	100.0	6301	US-09-891-685A-6	Sequence 6, Appl
C 14	20	100.0	7714	US-09-276-820A-26	Sequence 26, Appl
C 15	20	100.0	8031	US-09-850-716A-254	Sequence 254, Appl
C 16	20	100.0	8592	US-09-666-238-3	Sequence 3, Appl
C 17	20	100.0	12980	US-09-963-433-5	Sequence 5, Appl
C 18	20	100.0	413	US-09-933-524A-80149	Sequence 80149, A
C 19	20	100.0	419	US-09-933-524A-26906	Sequence 26906, A
C 20	20	100.0	440	US-09-933-524A-98104	Sequence 98104, A
C 21	20	100.0	475	US-09-933-524A-11298	Sequence 11298, A
C 22	20	100.0	475	US-09-898-888A-3832	Sequence 3832, A
C 23	20	100.0	559	US-09-922-279A-1645	Sequence 1645, A
C 24	20	100.0	923	US-09-965-529-68	Sequence 68, Appl
C 25	20	100.0	1102	US-09-719-961-1	Sequence 1, Appl
C 26	20	100.0	1215	US-09-719-961-1	Sequence 1, Appl

C 27	16.4	82.0	3395	US-09-898-888A-14401	Sequence 14401, A
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C 29	15.8	79.0	259	US-09-983-402-1660	Sequence 1660, A
C 30	15.8	79.0	592	US-09-922-279A-1036	Sequence 1036, A
C 31	15.8	79.0	954	US-09-880-729-1	Sequence 1, Appl
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C 33	15.8	79.0	3437	US-09-895-211-3	Sequence 3, Appl
C 34	15.8	79.0	13345	US-09-815-264-61249	Sequence 61249, A
C 35	15.8	79.0	14139	US-09-922-279A-4	Sequence 4, Appl
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C 40	15.4	77.0	272	US-09-985-678-292739	Sequence 292739, A
C 41	15.4	77.0	364	US-09-985-678-244601	Sequence 244601, A
C 42	15.4	77.0	1109	US-09-760-446A-934	Sequence 934, A
C 43	15.4	77.0	5154	US-09-815-264-90237	Sequence 90237, A
C 44	15.4	77.0	25978	US-09-815-264-65273	Sequence 65273, A
C 45	15.2	76.0	211	US-09-388-906A-19325	Sequence 19325, A

## ALIGNMENTS

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US-09-689-913-25/c  
Sequence 25, Application US/09689913  
GENERAL INFORMATION:  
APPLICANT: Iztusu, Hiroshi  
APPLICANT: Obara, Kazuhiko  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING  
THEROPR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O  
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUR  
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND  
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND  
TITLE OF INVENTION: PNEUMONIAE GENE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/689,913  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,326  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106006/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106008/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106009/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106010/95  
FILING DATE: 28-APR-1995

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Page 2

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106011/95  
FILING DATE: 28-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Charles E.  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 7426-043-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 669-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5438 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid; Plasmid  
US-09-689-913-25

Query Match  
Best Local Similarity 100.0%; Score 20; DB 6; Length 5438;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaactgactggtgaagc 20  
|||||  
DB 1694 GAGCTGACTGGTGAAGGC 1675

RESULT 2  
US-09-689-914-25/c  
Sequence 25, Application US/09689914  
GENERAL INFORMATION:  
APPLICANT: Izutsu, Hiroshi  
APPLICANT: Obara, Kazuhiko  
APPLICANT: Matsumoto, Akira  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING  
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF  
TITLE OF INVENTION: ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR  
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND  
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/689,914  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,326  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106006/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106008/95  
FILING DATE: 28-APR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106009/95  
FILING DATE: 28-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Charles E.  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 7426-043-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 669-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5438 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid; Plasmid  
US-09-689-914-25

Query Match  
Best Local Similarity 100.0%; Score 20; DB 6; Length 5438;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaactgactggtgaagc 20  
|||||  
DB 1694 GAGCTGACTGGTGAAGGC 1675

RESULT 3  
US-09-689-916-25/c  
Sequence 25, Application US/09689916  
GENERAL INFORMATION:  
APPLICANT: Izutsu, Hiroshi  
APPLICANT: Obara, Kazuhiko  
APPLICANT: Matsumoto, Akira  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, DNAS CODING  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING  
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF  
TITLE OF INVENTION: ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND  
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND  
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/689,916  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,326  
FILING DATE:



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106006/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106008/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106009/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106010/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106011/95  
FILING DATE: 28-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLER, Charles E.  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 7426-043-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5438 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid; Plasmid  
US-09-689-916-25

Query Match 100.0%; Score 20; DB 6; Length 5438;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttggaagc 20  
|||||  
Db 1694 GAGCTGACTGGGTGAAGC 1675

RESULT 4  
US-09-891-685A-4  
Sequence 4, Application US/09891685A  
GENERAL INFORMATION:  
APPLICANT: NORPHARMA SPA  
TITLE OF INVENTION: Recombinant bacterial strains for the production of  
TITLE OF INVENTION: natural nucleosides and modified analogues thereof  
FILE REFERENCE: 99PC26E  
CURRENT APPLICATION NUMBER: US/09/891,685A  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: M198A002792  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 5495  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Plasmid  
NAME/KEY: gene  
LOCATION: (231)..(960)  
OTHER INFORMATION: deod  
NAME/KEY: gene  
LOCATION: (1423)..(2822)  
OTHER INFORMATION: tetracycline resistance  
US-09-891-685A-4

Query Match 100.0%; Score 20; DB 6; Length 5495;  
Best Local Similarity 100.0%; Pred. No. 2.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 gagctgactgggttggaagc 20  
|||||  
Db 2162 gagctgactgggttggaagc 2181

RESULT 5  
US-09-891-685A-2  
Sequence 2, Application US/09891685A  
GENERAL INFORMATION:  
APPLICANT: NORPHARMA SPA  
TITLE OF INVENTION: Recombinant bacterial strains for the production of  
TITLE OF INVENTION: natural nucleosides and modified analogues thereof  
FILE REFERENCE: 99PC26E  
CURRENT APPLICATION NUMBER: US/09/891,685A  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: M198A002792  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 5556  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Plasmid  
NAME/KEY: gene  
LOCATION: (243)..(1021)  
OTHER INFORMATION: udp  
NAME/KEY: gene  
LOCATION: (1483)..(2883)  
OTHER INFORMATION: tetracycline resistance  
US-09-891-685A-2

Query Match 100.0%; Score 20; DB 6; Length 5556;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttggaagc 20  
|||||  
Db 2223 gagctgactgggttggaagc 2242

RESULT 6  
US-09-689-913-10/C  
Sequence 10, Application US/09689913  
GENERAL INFORMATION:  
APPLICANT: Izutsu, Hiroshi  
APPLICANT: Odara, Kazuhiko  
APPLICANT: Matsumoto, Akira  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES,  
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAs, TRANSFORMA  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O  
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA  
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND  
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND  
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA  
TITLE OF INVENTION: PNEUMONIAE GENE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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us-09-631-709-2.inpu

Page 4

OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30  
APPLICATION NUMBER: US/09/689,913  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,326  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106006/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106008/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106009/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106010/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106011/95  
FILING DATE: 28-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Charles E.  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 7426-043-999  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5658 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid; Plasmid  
US-09-689-913-10

Query Match  
Best Local Similarity 100.0%; Score 20; DB 6; Length 5658;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactgggtgaagc 20  
DB 1914 GAGCTGACTGGGTGAAGC 1895

RESULT 7  
US-09-689-914-10/c  
Sequence 10, Application US/09689914  
GENERAL INFORMATION:  
APPLICANT: Izutsu, Hiroshi  
APPLICANT: Obara, Kazuhiko  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING  
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF  
TITLE OF INVENTION: ANTI-BODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF ANTI-BODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR  
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA  
TITLE OF INVENTION: PNEUMONIAE GENE, AND METHOD AND  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30  
APPLICATION NUMBER: US/09/689,914  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,326  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106006/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106008/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106009/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106010/95  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 106011/95  
FILING DATE: 28-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Charles E.  
REGISTRATION NUMBER: 24,576  
REFERENCE/DOCKET NUMBER: 7426-043-999  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5658 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid; Plasmid  
US-09-689-914-10

Query Match  
Best Local Similarity 100.0%; Score 20; DB 6; Length 5658;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactgggtgaagc 20  
DB 1914 GAGCTGACTGGGTGAAGC 1895

RESULT 8  
US-09-689-916-10/c  
Sequence 10, Application US/09689916  
GENERAL INFORMATION:  
APPLICANT: Izutsu, Hiroshi  
APPLICANT: Obara, Kazuhiko  
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,  
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING  
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA  
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O  
TITLE OF INVENTION: ANTI-BODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF ANTI-BODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT  
TITLE OF INVENTION: OF PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND  
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA  
TITLE OF INVENTION: PNEUMONIAE GENE, AND METHOD AND

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; TITLE OF INVENTION: PNEUMONIAE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/689,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,326
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106006/95
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106008/95
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106009/95
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106010/95
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106011/95
; FILING DATE: 28-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7426-043-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid: Plasmid
; US-09-689-916-10

Query Match          100.0%; Score 20; DB 6; Length 5658;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttggaagc 20
    |||
Db 1914 GAGCTGACTGCGTTGAAGC 1895

RESULT 9
US-09-891-685A-8
; Sequence 8, Application US/09891685A
; GENERAL INFORMATION:
; APPLICANT: NORPARMA SPA
; TITLE OF INVENTION: Recombinant bacterial strains for the production of
; TITLE OF INVENTION: natural nucleosides and modified analogues thereof
; FILE REFERENCE: 99DC26E
; CURRENT APPLICATION NUMBER: US/09/891,685A
; CURRENT FILING DATE: 2001-06-25
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; PRIOR APPLICATION NUMBER: M198A002792
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pgm716 with
; OTHER INFORMATION: deletion of HpaI fragment
US-09-891-685A-8

Query Match          100.0%; Score 20; DB 6; Length 5822;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttggaagc 20
    |||
Db 2489 gagctgactggttggaagc 2508

RESULT 10
US-09-891-685A-15
; Sequence 15, Application US/09891685A
; GENERAL INFORMATION:
; APPLICANT: NORPARMA SPA
; TITLE OF INVENTION: Recombinant bacterial strains for the production of
; TITLE OF INVENTION: natural nucleosides and modified analogues thereof
; FILE REFERENCE: 99DC26E
; CURRENT APPLICATION NUMBER: US/09/891,685A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: M198A002792
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 6046
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: udp and deod
; OTHER INFORMATION: cloned downstream plac promoter
US-09-891-685A-15

Query Match          100.0%; Score 20; DB 6; Length 6046;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttggaagc 20
    |||
Db 2926 gagctgactggttggaagc 2945

RESULT 11
US-09-611-451-51/C
; Sequence 51, Application US/09611451
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; BURTON, Dennis R.
; LERNER, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10550 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
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Fri Dec 14 09:21:16 2001

us-09-631-709-2.inpn

Page 6

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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,153
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784,2937
TELEFAX: (619) 784,3399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-611-451-51
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 6166;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 656 GAGCTGACTGGTGAAGC 637
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RESULT 12
US-09-891-685A-9
Sequence 9, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
PRIORITY FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 9
LENGTH: 6269
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: udp and deod
OTHER INFORMATION: cloned in pUC18 so to create a fusion between the
US-09-891-685A-9
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 6269;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gagctgactggttgaagc 20
DB 2936 gagctgactggttgaagc 2955
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RESULT 13
US-09-891-685A-10
Sequence 10, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
PRIORITY FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 10
LENGTH: 6299
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: udp and deod
OTHER INFORMATION: cloned in pUC18 so to create a fusion between the
US-09-891-685A-10
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 6299;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 2966 gagctgactggttgaagc 2985
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RESULT 14
US-09-891-685A-6
Sequence 6, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
PRIORITY FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 6301
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Plasmid
LOCATION: (243)..(1021)
NAME/KEY: gene
LOCATION: (1037)..(1766)
OTHER INFORMATION: deod
NAME/KEY: gene
LOCATION: (2229)..(3628)
OTHER INFORMATION: tetracycline resistance
US-09-891-685A-6
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 6301;
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Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20  
|||||  
Db 2968 gagctgactggttgaagc 2987

RESULT 15

US-09-276-820A-26  
; Sequence 26, Application US/09276820A  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; FILE REFERENCE: 0221-0003US  
; CURRENT APPLICATION NUMBER: US/09/276,820A  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 7714  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-276-820A-26

Query Match 100.0%; Score 20; DB 6; Length 7714;

Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20  
|||||  
Db 791 gagctgactggttgaagc 810

Search completed: December 13, 2001, 19:14:05  
Job time: 20479 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 18:29:30 : Search time 9967.36 Seconds  
(without alignments)  
35.168 Million cell updates/sec

Title: US-09-631-709-2  
Perfect score: 20  
Sequence: 1 gagctgactggttgtaagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 17159718 seqs, 8763200856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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18:	/cgn2_6/ptodata/2/pna/US0628.COMB.seq:*
19:	/cgn2_6/ptodata/2/pna/US0629.COMB.seq:*
20:	/cgn2_6/ptodata/2/pna/US0630.COMB.seq:*
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23:	/cgn2_6/ptodata/2/pna/US0633.COMB.seq:*
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25:	/cgn2_6/ptodata/2/pna/US0635.COMB.seq:*
26:	/cgn2_6/ptodata/2/pna/US0636.COMB.seq:*
27:	/cgn2_6/ptodata/2/pna/US0637.COMB.seq:*
28:	/cgn2_6/ptodata/2/pna/US0638.COMB.seq:*
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38:	/cgn2_6/ptodata/2/pna/US0648.COMB.seq:*
39:	/cgn2_6/ptodata/2/pna/US0649.COMB.seq:*
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	24	US-09-631-709-2
2	20	100.0	169	11	US-08-781-966A-2722
3	20	100.0	169	13	US-08-956-171-2722
4	20	100.0	169	13	US-08-956-171B-2722
5	20	100.0	169	13	US-08-956-171C-2722
6	20	100.0	185	31	US-09-834-366-32199
7	20	100.0	185	52	US-60-197-873-32199
8	20	100.0	243	51	US-60-182-316-11146
9	20	100.0	294	12	US-08-808-443A-2457
10	20	100.0	294	12	US-08-880-314-881
11	20	100.0	294	34	US-60-012-233-2457
12	20	100.0	689	56	US-60-233-942-25
13	20	100.0	751	56	US-60-233-942-36
14	20	100.0	794	1	PCT-US01-01338-5573
15	20	100.0	794	1	PCT-US01-01339-5603
16	20	100.0	794	30	US-09-764-891-5573
17	20	100.0	807	1	PCT-US01-08656-1603
18	20	100.0	807	1	PCT-US01-14827-541
19	20	100.0	807	22	US-09-577-408-1501
20	20	100.0	863	56	US-60-233-942-13
21	20	100.0	994	1	PCT-US01-01328-447
22	20	100.0	994	1	PCT-US01-01328A-447
23	20	100.0	1140	8	US-08-406-801-18
24	20	100.0	1140	1	US-08-406-801-33
25	20	100.0	1146	8	PCT-US01-08631-3887
26	20	100.0	1459	32	US-09-950-082-1751
27	20	100.0	1533	1	PCT-US01-08631-10386
28	20	100.0	1533	1	PCT-US01-08631-24078
29	20	100.0	1632	1	PCT-US01-14827-2872
30	20	100.0	1632	22	US-09-577-408-3816
31	20	100.0	1883	1	PCT-US01-08631-24063
32	20	100.0	1883	1	PCT-US01-14827-2862
33	20	100.0	1983	22	US-09-577-408-3807
34	20	100.0	2106	1	PCT-US01-14827-2881
35	20	100.0	2106	22	US-09-577-408-3824
36	20	100.0	2124	1	PCT-US01-08631-10378
37	20	100.0	2124	1	PCT-US01-08631-24067
38	20	100.0	2126	1	PCT-US01-08631-24087
39	20	100.0	2562	1	PCT-US01-08631-24085
40	20	100.0	2562	1	PCT-US01-14827-2251
41	20	100.0	2562	1	PCT-US01-14827-2251

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Page 2

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C 43 20 100.0 2607 1 PCT-US01-08631-10418  
C 44 20 100.0 2607 1 PCT-US01-08631-10418  
C 45 20 100.0 2607 1 PCT-US01-14827-2884

Sequence 3188, Ap  
Sequence 10418, A  
Sequence 10418, A  
Sequence 24075, A  
Sequence 2884, Ap

ALIGNMENTS

RESULT 1  
US-09-631-709-2  
; Sequence 2, Application US/09631709  
; GENERAL INFORMATION:  
; APPLICANT: KIOMA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: PROCESS FOR PRODUCING GDP-FUCOSE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/631,709  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver.2.0  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-631-709-2

Query Match 100.0%; Score 20; DB 24; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20  
Db 1 gagctgactgggttgaagc 20

RESULT 2  
US-08-781-986A-2722  
; Sequence 2722, Application US/08781986A  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; OPERATING SYSTEM: HP Vectra 486/33  
; SOFTWARE: MSDOS version 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248BP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 2722:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 169 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2722

Query Match 100.0%; Score 20; DB 11; Length 169;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20  
Db 112 GAGCTGACTGGGTGGAAGC 131

RESULT 3  
US-08-956-171-2722  
; Sequence 2722, Application US/08956171  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; OPERATING SYSTEM: HP Vectra 486/33  
; SOFTWARE: MSDOS version 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248BP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 2722:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-956-171-2722

Query Match 100.0%; Score 20; DB 13; Length 169;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20  
Db 112 GAGCTGACTGGGTGGAAGC 131

RESULT 4  
US-08-956-171B-2722  
; Sequence 2722, Application US/08956171B  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; GIL H. Choi



Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171B  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 610-5790  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 2722:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2722:  
US-08-956-171B-2722  
Query Match 100.0%; Score 20; DB 13; Length 169;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
|||||  
Db 112 GAGCTGACTGCGTTGAAGC 131  
RESULT 5  
US-08-956-171C-2722  
Sequence 2722, Application US/08956171C  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171C  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 610-5790  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 2722:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2722:  
US-08-956-171C-2722  
Query Match 100.0%; Score 20; DB 13; Length 169;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
|||||  
Db 112 GAGCTGACTGCGTTGAAGC 131  
RESULT 6  
US-09-834-366-32199  
Sequence 32199, Application US/09834366  
GENERAL INFORMATION:  
APPLICANT: Benjamin, Stephane  
Tanaka, Hiroaki  
Dumas Milne Edwards, Jean Baptiste  
APPLICANT: Jobert, Severin  
Giordano, Jean-Yves  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: 81 US2, REG  
CURRENT APPLICATION NUMBER: US/09/834,366  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: US 60/197,873  
PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 52153  
SOFTWARE: Patent.pm  
SEQ ID NO 32199  
LENGTH: 185  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-834-366-32199  
Query Match 100.0%; Score 20; DB 31; Length 185;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
|||||  
Db 10 gagctgactggttgaagc 29  
RESULT 7

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US-60-197-873-32199
; Sequence 32199
; GENERAL INFORMATION:
; APPLICATION: Application US/60197873
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas, Milne Edwards, Jean Baptiste
; APPLICANT: Giordano, Jean Yves
; TITLE OF INVENTION: SRS and Encoded Human Proteins.
; FILE REFERENCE: 81 US PRO
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 32199
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-197-873-32199

Query Match
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
DB 10 gagctgactgggttgaagc 29

RESULT 8
; Sequence 11146
; GENERAL INFORMATION:
; APPLICATION: Application US/60182316
; APPLICANT: Curtis, Anne L.
; APPLICANT: Lagace, Robert E.
; APPLICANT: Klingler, Tod M.
; APPLICANT: Scuve, Laura L.
; TITLE OF INVENTION: CPG Island Polynucleotides
; FILE REFERENCE: PX-0003 P
; CURRENT APPLICATION NUMBER: US/60/182,316
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 14,630
; SOFTWARE: IREL Program
; SEQ ID NO 11146
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: CPG_991027_B15_masked_fa.Contig36197
US-60-182-316-11146

Query Match
Best Local Similarity 100.0%; Score 20; DB 51; Length 243;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
DB 178 gagctgactgggttgaagc 197

RESULT 9
; Sequence 2457
; GENERAL INFORMATION:
; APPLICATION: Application US/08808443A
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura Y.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerdlom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
US-08-808-443A-2457/C

US-08-808-443A-2457
; Sequence 881
; GENERAL INFORMATION:
; APPLICATION: Application US/0880314
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura Y.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerdlom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN
; NUMBER OF SEQUENCES: 4685
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,443A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: FISHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PD 0117P
; TELECOMMUNICATIONS INFORMATION:
; TELEPHONE: (415) 852-0555
; TELEFAX: (415) 852-0195
; INFORMATION FOR SEQ ID NO 2457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 831577
US-08-808-443A-2457

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 294;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
DB 21 GAGCTGACTGGGTGAAGC 2

RESULT 10
; Sequence 881
; GENERAL INFORMATION:
; APPLICATION: Application US/0880314
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura Y.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerdlom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 4685
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,314  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/020,415  
FILING DATE: JUNE 24, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/025,817  
FILING DATE: SEPTEMBER 5, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/808,443  
FILING DATE: FEBRUARY 26, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0197 US  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 881:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 831577  
US-08-880-314-881

Query Match 100.0%; Score 20; DB 12; Length 294;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20  
|||||  
DB 21 GAGCTGACTGGTTGAAGC 2

RESULT 11  
US-60-012-233-2457/c  
Sequence 2457, Application US/60012233  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerbom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN  
TITLE OF INVENTION: PROSTATE  
NUMBER OF SEQUENCES: 3111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/012,233

FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PD 0117P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 852-0195  
INFORMATION FOR SEQ ID NO: 2457:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 831577  
US-60-012-233-2457

Query Match 100.0%; Score 20; DB 34; Length 294;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20  
|||||  
DB 21 GAGCTGACTGGTTGAAGC 2

RESULT 12  
US-60-233-942-25/c  
Sequence 25, Application US/60233942  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN PHASE II  
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF  
FILE REFERENCE: C1000825  
CURRENT APPLICATION NUMBER: US/60/233,942  
CURRENT FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 689  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(689)  
OTHER INFORMATION: n = A,T,C or G  
US-60-233-942-25

Query Match 100.0%; Score 20; DB 56; Length 689;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20  
|||||  
DB 48 GAGCTGACTGGTTGAAGC 29

RESULT 13  
US-60-233-942-36/c  
Sequence 36, Application US/60233942  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN PHASE II  
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF  
FILE REFERENCE: C1000825  
CURRENT APPLICATION NUMBER: US/60/233,942

Fri Dec 14 09:21:16 2001

us-09-631-709-2.rnp

CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 210
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 751
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(751)
OTHER INFORMATION: n = A,T,C or G
US-60-233-942-36

Db
756 gagctgactggttgaagc 775

Search completed: December 13, 2001, 18:29:31
Job time: 18165 sec

Query Match
Best Local Similarity 100.0%; Score 20; DB 56; Length 751;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gagctgactggttgaagc 20
Db 313 GAGCTGACTGGGTGAAGCC 294

RESULT 14
PCT-US01-01339-5573
Sequence 5573, Application PC/TUS0101339
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5573
LENGTH: 794
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-01339-5573

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 794;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gagctgactggttgaagc 20
Db 756 gagctgactggttgaagc 775

RESULT 15
PCT-US01-01339-5603
Sequence 5603, Application PC/TUS0101339
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5603
LENGTH: 794
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-01339-5603

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 794;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gagctgactggttgaagc 20



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 13:29:57 ; Search time 176.03 Seconds  
(without alignments)  
25.732 Million cell updates/sec

Title: US-09-631-709-2  
Perfect score: 20  
Sequence: 1 gagctgactggttggaagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/pdata/2/1na/5B.COMB.seq:\*  
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4: /cgn2\_6/pdata/2/1na/6B.COMB.seq:\*  
5: /cgn2\_6/pdata/2/1na/PTUS.COMB.seq:\*  
6: /cgn2\_6/pdata/2/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	41	3	US-08-973-965-1 Sequence 1, Appl
2	20	100.0	92	3	US-08-973-965-3 Sequence 3, Appl
3	20	100.0	95	3	US-08-973-965-39 Sequence 39, Appl
4	20	100.0	710	3	US-09-098-287A-5 Sequence 5, Appl
5	20	100.0	1130	2	US-08-613-965-1 Sequence 1, Appl
6	20	100.0	1130	2	US-08-918-966-1 Sequence 1, Appl
7	20	100.0	1130	3	US-08-921-655-1 Sequence 1, Appl
8	20	100.0	1140	1	US-08-218-303-15 Sequence 15, Appl
9	20	100.0	1140	2	US-08-338-793D-60 Sequence 60, Appl
10	20	100.0	3301	2	US-08-447-430A-42 Sequence 42, Appl
11	20	100.0	3423	2	US-08-447-430A-40 Sequence 40, Appl
12	20	100.0	3474	2	US-08-447-430A-41 Sequence 41, Appl
13	20	100.0	3474	2	US-08-318-837-10 Sequence 10, Appl
14	20	100.0	4009	2	US-08-500-860A-2 Sequence 2, Appl
15	20	100.0	4245	2	US-08-929-967-4 Sequence 4, Appl
16	20	100.0	4309	5	PCT-US91-02954-11 Sequence 11, Appl
17	20	100.0	4593	4	US-08-801-344-1 Sequence 1, Appl
18	20	100.0	4593	4	US-09-498-599-1 Sequence 1, Appl
19	20	100.0	4819	1	US-08-450-257-20 Sequence 20, Appl
20	20	100.0	4819	1	US-08-450-246-20 Sequence 20, Appl
21	20	100.0	4819	1	US-08-450-098-20 Sequence 20, Appl
22	20	100.0	4819	1	US-08-451-233-20 Sequence 20, Appl
23	20	100.0	4819	1	US-08-450-236-20 Sequence 20, Appl
24	20	100.0	4810	1	US-08-450-257-11 Sequence 11, Appl
25	20	100.0	4910	1	US-08-450-246-11 Sequence 11, Appl
26	20	100.0	4910	1	US-08-450-098-11 Sequence 11, Appl
27	20	100.0	4910	1	US-08-451-233-11 Sequence 11, Appl

28	20	100.0	4910	1	US-08-450-236-11 Sequence 11, Appl
29	20	100.0	4977	1	US-08-450-257-14 Sequence 14, Appl
30	20	100.0	4977	1	US-08-450-257-17 Sequence 17, Appl
31	20	100.0	4977	1	US-08-450-246-14 Sequence 14, Appl
32	20	100.0	4977	1	US-08-450-246-17 Sequence 17, Appl
33	20	100.0	4977	1	US-08-450-098-14 Sequence 14, Appl
34	20	100.0	4977	1	US-08-450-098-17 Sequence 17, Appl
35	20	100.0	4977	1	US-08-451-233-14 Sequence 14, Appl
36	20	100.0	4977	1	US-08-451-233-17 Sequence 17, Appl
37	20	100.0	4977	1	US-08-450-236-17 Sequence 17, Appl
38	20	100.0	4977	1	US-08-450-236-17 Sequence 17, Appl
39	20	100.0	4990	3	US-08-776-511-1 Sequence 1, Appl
40	20	100.0	5098	1	US-08-450-257-10 Sequence 10, Appl
41	20	100.0	5098	1	US-08-450-246-10 Sequence 10, Appl
42	20	100.0	5098	1	US-08-450-098-10 Sequence 10, Appl
43	20	100.0	5098	1	US-08-451-233-10 Sequence 10, Appl
44	20	100.0	5098	1	US-08-450-236-10 Sequence 10, Appl
45	20	100.0	5115	3	US-08-825-852-19 Sequence 19, Appl

## ALIGNMENTS

```
RESULT 1
US-08-973-965-1/c
; Sequence 1, Application US/08973965
; Patent No. 6033881
; GENERAL INFORMATION:
; APPLICANT: HIMMELER, Gottfried
; APPLICANT: SCHLEDERER, Thomas
; TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
; FILE REFERENCE: 030560-055
; CURRENT APPLICATION NUMBER: US/08/973,965
; EARLIER FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: AT A 1007/95
; EARLIER FILING DATE: 1995-06-13
; EARLIER APPLICATION NUMBER: PCT/AT96/00106
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 41
; TYPE: DNA
; ORGANISM: synthetic construct
US-08-973-965-1

Query Match          100.0%; Score 20; DB 3; Length 41;
Best local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttggaagc 20
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DB 23 GAGCTGACTGCTTGAAGGC 4

RESULT 2
US-08-973-965-3/c
; Sequence 3, Application US/08973965
; Patent No. 6033881
; GENERAL INFORMATION:
; APPLICANT: HIMMELER, Gottfried
; APPLICANT: SCHLEDERER, Thomas
; TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
; FILE REFERENCE: 030560-055
; CURRENT APPLICATION NUMBER: US/08/973,965
; EARLIER FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: AT A 1007/95
; EARLIER FILING DATE: 1995-06-13
; EARLIER APPLICATION NUMBER: PCT/AT96/00106
; EARLIER FILING DATE: 1996-06-13
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us-09-631-709-2.rn1

Page 2

NUMBER OF SEQ ID NOS: 41  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 92  
TYPE: DNA  
ORGANISM: synthetic construct  
US-08-973-965-3

Query Match  
Best Local Similarity 100.0%; Score 20; DB 3; Length 92;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20  
DB 23 GAGCTGACTGGTTGAAGC 4

RESULT 3  
US-08-973-965-39/C  
Sequence 39, Application US/08973965  
Patent No. 6033881  
GENERAL INFORMATION:  
APPLICANT: HIMLER, Gottfried  
APPLICANT: SCHLEDERER, Thomas  
TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF  
FILE REFERENCE: 030560-055  
CURRENT APPLICATION NUMBER: US/08/973,965  
EARLIER FILING DATE: 1998-04-06  
EARLIER APPLICATION NUMBER: AT 1007/95  
EARLIER FILING DATE: 1995-06-13  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 39  
LENGTH: 95  
TYPE: DNA  
ORGANISM: synthetic construct  
US-08-973-965-39

Query Match  
Best Local Similarity 100.0%; Score 20; DB 3; Length 95;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20  
DB 23 GAGCTGACTGGTTGAAGC 4

RESULT 4  
US-09-098-287A-5/C  
Sequence 5, Application US/09098287A  
Patent No. 6158950  
GENERAL INFORMATION:  
APPLICANT: BOTTION  
APPLICANT: Sodreback, Carl M.  
APPLICANT: Sodreback, Ulf, HE  
TITLE OF INVENTION: A method for in vitro molecular  
FILE REFERENCE: evolution of protein function  
CURRENT APPLICATION NUMBER: US/09/098,287  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: GB9712512.4  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 710  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Theoretical insert  
US-09-098-287A-5

Query Match  
Best Local Similarity 100.0%; Score 20; DB 3; Length 710;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20  
DB 461 GAGCTGACTGGTTGAAGC 442

RESULT 5  
US-08-613-965-1/C  
Sequence 1, Application US/08613965  
Patent No. 5916745  
GENERAL INFORMATION:  
APPLICANT: Robert M. Cook and Ahmed Raafat  
TITLE OF INVENTION: Method for Determination  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 Inch, 360 KB  
MEDIUM TYPE: Storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: NoSuperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/613,965  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-290  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1130  
TYPE: nucleotides  
STRANDEDNESS: Single  
MOLECULE TYPE: Linear  
DESCRIPTION: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bovine  
STRAIN:  
INDIVIDUAL ISOLATE: ATCS  
CELL TYPE: mammary gland  
FEATURE:  
NAME/KEY: CDNA in pATCS  
LOCATION: mammary gland CDNA and  
IDENTIFICATION METHOD: Sequencing  
OTHER INFORMATION: Encodes a portion  
of acetyl coenzyme A



OTHER INFORMATION: synthetase  
US-08-613-965-1

Query Match 100.0%; Score 20; DB 2; Length 1130;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaactgactgggtgaagc 20  
|||||  
DB 836 GAGCTGACTGGTGAAGC 817

## RESULT 6

US-08-918-966-1/c  
; Sequence 1, Application US/08918966  
; Patent No. 5981187  
; GENERAL INFORMATION:  
; APPLICANT: Robert M. Cook and Ahmed Raafat  
; TITLE OF INVENTION: Method For Determination  
; TITLE OF INVENTION: of Bovine Milk Production Potential  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/918,966  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: NO. 5981187e  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1130  
; TYPE: nucleotides  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: CDNA  
; DESCRIPTION: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bovine  
; STRAIN:  
; INDIVIDUAL ISOLATE: ATC5  
; CELL TYPE: mammary gland  
; FEATURE:  
; NAME/KEY: CDNA in PATC5  
; LOCATION: mammary gland CDNA and  
; LOCATION: encoded peptide  
; IDENTIFICATION METHOD: Sequencing  
; OTHER INFORMATION: Encodes a portion  
; OTHER INFORMATION: of acetyl coenzyme A  
; OTHER INFORMATION: synthetase

US-08-918-966-1

Query Match 100.0%; Score 20; DB 2; Length 1130;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaactgactgggtgaagc 20  
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DB 836 GAGCTGACTGGTGAAGC 817

## RESULT 7

US-08-921-655-1/c  
; Sequence 1, Application US/08921655  
; Patent No. 6013496  
; GENERAL INFORMATION:  
; APPLICANT: Robert M. Cook and Ahmed Raafat  
; TITLE OF INVENTION: Method For Determination  
; TITLE OF INVENTION: of Bovine Milk Production Potential  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/921,655  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: NO. 6013496e  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1130  
; TYPE: nucleotides  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: CDNA  
; DESCRIPTION: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bovine  
; STRAIN:  
; INDIVIDUAL ISOLATE: ATC5  
; CELL TYPE: mammary gland  
; FEATURE:  
; NAME/KEY: CDNA in PATC5  
; LOCATION: mammary gland CDNA and  
; LOCATION: encoded peptide  
; IDENTIFICATION METHOD: Sequencing  
; OTHER INFORMATION: Encodes a portion  
; OTHER INFORMATION: of acetyl coenzyme A  
; OTHER INFORMATION: synthetase  
US-08-921-655-1

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us-09-631-709-2.rn1

Page 4

Query Match 100.0%; Score 20; DB 3; Length 1130;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttaagc 20  
DB 836 GAGCTGACTGCTTGAAGC 817

RESULT 8  
US-08-218-303-15/c  
Sequence 15, Application US/08218303  
Patent No. 5547867  
GENERAL INFORMATION:  
APPLICANT: Kara, Bhupendra V.  
APPLICANT: Hockney, Robert C.  
TITLE OF INVENTION: FERMENTATION PROCESS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cushman, Darby & Cushman  
STREET: 1615 L Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,303  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/841,533  
FILING DATE: 26-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kokulis, Paul N.  
REGISTRATION NUMBER: 16,773  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1140 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 143..943  
US-08-218-303-15

Query Match 100.0%; Score 20; DB 1; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttaagc 20  
DB 1076 GAGCTGACTGCTTGAAGC 1057

RESULT 9  
US-08-338-793D-60/c  
Sequence 60, Application US/08338793D

Patent No. 5840521  
GENERAL INFORMATION:  
APPLICANT: Barth, Peter Thomas  
TITLE OF INVENTION: VECTOR  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY CUSHMAN  
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.50 inch, 1.44 MB storage  
COMPUTER: IBM PC/XT/AT Compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word or ASCII editors  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,793D  
FILING DATE: 08 MAR 5840521-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842,081  
FILING DATE: 26-Feb-92  
CLASSIFICATION: 435  
APPLICATION NUMBER: 9104017.0  
FILING DATE: 26-Feb-91  
APPLICATION NUMBER: 9109188.4  
ATTORNEY/AGENT INFORMATION:  
NAME: Kokulis, Paul N.  
REGISTRATION NUMBER: 16,773  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1140  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-338-793D-60

Query Match 100.0%; Score 20; DB 2; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttaagc 20  
DB 1076 GAGCTGACTGCTTGAAGC 1057

RESULT 10  
US-08-447-430A-42  
Sequence 42, Application US/08447430A  
Patent No. 5916558  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Recombinant polypeptides and peptides,  
nucleic acids coding for the same and use of these  
TITLE OF INVENTION: polypeptides and peptides in the diagnostic of  
NUMBER OF SEQUENCES: 43  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
;
US-08-447-430A-42

Query Match          100.0%; Score 20; DB 2; Length 3301;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
    |||
Db 2612 GAGCTGACTGGGTTGAAGC 2631

RESULT 11
US-08-447-430A-40
; Sequence 40, Application US/08447430A
; Patent No. 5916558
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
;
US-08-447-430A-40

Query Match          100.0%; Score 20; DB 2; Length 3423;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
    |||
Db 2730 GAGCTGACTGGGTTGAAGC 2749

RESULT 12
US-08-447-430A-41
; Sequence 41, Application US/08447430A
; Patent No. 5916558
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
```

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; TITLE OF INVENTION: tuberculosis.
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
;
US-08-447-430A-41

Query Match          100.0%; Score 20; DB 2; Length 3474;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
    |||
Db 2783 GAGCTGACTGGGTTGAAGC 2802

RESULT 13
US-08-318-837-10
; Sequence 10, Application US/08318837
; Patent No. 5981277
; GENERAL INFORMATION:
; APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
; APPLICANT: ANDRE; VAN HEUVERSWEY, HUGO
; TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
; TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAP
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,837
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 93/01022
; FILING DATE: 28-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 92.401.231.3
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
```

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us-09-631-709-2.rni

LENGTH: 3474 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: pMTNF-MPH  
US-08-318-837-10

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 3474;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
DB 2783 GAGCTGACTGGTTGAAGC 2802

RESULT 14  
US-08-500-860A-2  
Sequence 2, Application US/08500860A  
Patent No. 5891678  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BERTSELIER, PATRICK  
APPLICANT: PRANSEN, LUCIE  
TITLE OF INVENTION: TNF-MUTAINS, A PROCESS FOR PREPARING THEM AND  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: NIXON & VANDERHUYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
TELECOMMUNICATION INFORMATION: 1487-8  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4009 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: PIG2  
US-08-500-860A-2

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 4009;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
DB 3320 GAGCTGACTGGTTGAAGC 3339

RESULT 15  
US-08-929-967-4/C  
Sequence 4, Application US/08929967  
Patent No. 5891637  
GENERAL INFORMATION:  
APPLICANT: Ruppert, Siegfried J.W.  
TITLE OF INVENTION: Construction of Full-Length cDNA Libraries  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MIMAS (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,967  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
TELECOMMUNICATION INFORMATION: P1035R1  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4245 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-929-967-4

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 4245;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gagctgactggttgaagc 20  
DB 2185 GAGCTGACTGGTTGAAGC 2166

Search completed: December 13, 2001, 13:29:59  
Job time: 193 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:43:08 ; Search time 496.49 Seconds  
(without alignments)  
34.535 Million cell updates/sec

Title: US-09-631-709-2

Perfect score: 20

Sequence: 1 gagctgactggttgaaagc 20.

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_1101:\*

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4:	/SIDS2/gcgcgdata/geneseq/geneseqn/NA1983.DAT:*
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21:	/SIDS2/gcgcgdata/geneseq/geneseqn/NA2000.DAT:*
22:	/SIDS2/gcgcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AAH46615	Synthetic oligonuc
2	20	100.0	20	AAF62503	Primer for gik gen
3	20	100.0	41	AAT36954	Primer used in tra
4	20	100.0	41	AAT36970	Oligonucleotide us
5	20	100.0	41	AAT36971	Oligonucleotide us
6	20	100.0	91	AAT36956	Template used in t
7	20	100.0	91	AAF36974	Template used in t
8	20	100.0	169	AAV77033	Staphylococcus aur
9	20	100.0	600	AAH60881	Sequence encoding
10	20	100.0	600	AAH60882	Sequence encoding
11	20	100.0	710	AAH00997	Mutated tetracycli

C	12	20	100.0	1097	21	AAZ34980
C	13	20	100.0	1130	20	AAZ35503
C	14	20	100.0	1130	21	AAZ87413
C	15	20	100.0	1140	13	AAO27876
C	16	20	100.0	1140	14	AAO36947
C	17	20	100.0	1632	11	AAO03698
C	18	20	100.0	3000	7	AAH60892
C	19	20	100.0	3000	8	AAH60892
C	20	20	100.0	3327	22	AAH62653
C	21	20	100.0	3369	22	AAH62655
C	22	20	100.0	3423	12	AAO11083
C	23	20	100.0	3423	20	AAH08615
C	24	20	100.0	3474	13	AAO29146
C	25	20	100.0	3474	14	AAO51546
C	26	20	100.0	3880	22	AAE25570
C	27	20	100.0	3954	22	AAH62660
C	28	20	100.0	3976	22	AAH62656
C	29	20	100.0	3985	16	AAO81201
C	30	20	100.0	4009	15	AAO70219
C	31	20	100.0	4163	21	AAO29134
C	32	20	100.0	4196	21	AAA30825
C	33	20	100.0	4207	10	AAH92031
C	34	20	100.0	4222	10	AAH92038
C	35	20	100.0	4269	21	AAA92002
C	36	20	100.0	4300	21	AAA29135
C	37	20	100.0	4369	21	AAZ9578
C	38	20	100.0	4464	22	AAH62664
C	39	20	100.0	4466	10	AAH90286
C	40	20	100.0	4466	15	AAO58637
C	41	20	100.0	4586	19	AAV43441
C	42	20	100.0	4608	10	AAH90288
C	43	20	100.0	4643	13	AAO25112
C	44	20	100.0	4645	10	AAH92023
C	45	20	100.0	4651	10	AAH92044

#### ALIGNMENTS

RESULT 1

ID	AAH46615	standard: DNA: 20 BP.
AC	AAH46615:	
DT	17-SEP-2001 (first entry)	
DE	Synthetic oligonucleotide #18.	
KW	Helicobacter pylori: alpha-1,2-fucosyltransferase;	
KW	fucose-containing sugar production; Lewis antigen; ss.	
OS	Synthetic.	
PN	MO200146400-A1.	
PD	28-JUN-2001.	
PF	20-DEC-2000; 2000MO-TP09033.	
PR	21-DEC-1999; 99JP-0362243.	
PA	(KYOW) KYOMA HAKKO KOGYO KK.	
PI	Endo T, Koizumi S, Tabata K, Ozaki A;	
DR	WPI; 2001-418061/44.	
PT	Modified alpha-1,2-fucosyltransferase gene and its expression product	
PT	for efficient production of fucose-containing sugars such as Lewis	
PS	antigen -	
PS	Example 2; Page 62; 69pp; Japanese.	

Mouse F1271 expres  
Clone ATC 5 polyu  
Bovine acetyl coen  
Ricin A gene from  
Partial sequence o  
Recombinant plasm  
Sequence of plasm  
Sequence contg. ce  
Plasmid GHRH1-29YA  
pGHRH-4 44SK const  
Plasmid pIGR1 for  
pIGR12 expression  
pMNF-MPH plasmid  
Expression plasmid  
Vector pSRM4 DNA.  
Plasmid GHRH1-29YW  
pGHRH1-44WTSK685 c  
Plasmid pLPRS. S  
Plasmid pIG2 for T  
pNF-kappaB-d2EGFP  
Expression cassette  
Sequence of recomb  
Sequence of recomb  
pCRES-d2EGFP report  
pCRES-d2EGFP const  
Partial sequence o  
Plasmid GHRH1-29YA  
Plasmid pTP104-4.  
pTP104-4 sequence.  
DNA sequence of th  
Plasmid pTP70-1.  
DHFR-AP fusion pr  
Recombinant plasm  
Sequence of recomb

CC The invention relates to DNA encoding a modified form of the  
 CC alpha-1,2-fucosyltransferase of Helicobacter pylori. The  
 CC polycytosine sequence of the AAAAAG sequence and/or the  
 CC repeats has been modified in the DNA sequence and/or the number of TAA  
 CC useful in the production of large amounts of fucose-containing  
 CC sugars, such as Lewis x and Lewis y antigens for medicinal use. The present  
 CC sequence is an oligonucleotide provided in the specification.  
 SO Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 22; Length 20;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20  
 Db 1 gagctgactgggttgaaagc 20

RESULT 2

ID AAF62503 standard; DNA; 20 BP.  
 AC AAF62503;  
 DT 08-MAY-2001 (first entry)  
 DE Primer for glk gene.  
 KW Guanosine 5'-diphosphofucose; GDP-fucose;  
 KW Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDW; immunotherapy;  
 KW cardiovascular; infection; ss.  
 OS Synthetic.  
 PN EPI076096-A1.  
 PD 14-FEB-2001.  
 PF 10-AUG-2000; 2000EP-0117167.  
 PR 10-AUG-1999; 99JP-0225889.  
 PA (RYOW) KYOMA HAKKO KOGYO KK.  
 PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;  
 DR WPI; 2001-193203/20.  
 XX Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a  
 XX substrate of complex carbohydrates for immunotherapy comprises  
 XX employing microorganisms that convert guanosine  
 XX 5-diphospho-4-keto-6-deoxymannose to GDP-fucose -  
 PS Example 1; Page 11; 19pp; English.  
 CC The present invention relates to producing guanosine  
 CC 5'-diphosphofucose (GDP-fucose) by employing an enzyme source  
 CC that is a culture broth of microorganisms. GDP-fucose is useful  
 CC as a synthetic substrate of complex carbohydrates that are useful  
 CC diseases, or infections by bacteria or viruses. Cardiovascular  
 CC 5'-diphospho-4-keto-6-deoxymannose (GKDW) is useful as  
 CC an intermediate for the production of GDP-fucose.  
 SO Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 22; Length 20;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20  
 Db 1 gagctgactgggttgaaagc 20

RESULT 3

ID AAT36954 standard; DNA; 41 BP.  
 AC AAT36954;  
 DT 16-FEB-1997 (first entry)  
 DE Primer used in transcription free amplification method.  
 KW Amplification; primer; template; transcription; diagnosis;  
 KW medicine; environmental analysis; forensic analysis; ss.  
 OS Synthetic.  
 PN AT9501007-A.  
 PD 15-JUL-1996.  
 PF 13-JUN-1995; 95AT-0001007.  
 PR 13-JUN-1995; 95AT-0001007.  
 PA (HIMM) HIMMELER G.  
 DR WPI; 1996-322132/33.  
 XX Transcription free amplification of nucleic acid - with  
 XX amplification and strand sepn. of prod. at same temp.; useful for in  
 XX vitro clinical diagnosis  
 PS Example 1; Page 9; 25pp; German.  
 CC Transcription free amplification of a nucleic acid sequence (A) with  
 CC enzymes, comprises: (1) optionally, before amplification, converting  
 CC (A) at least partly to individual strands by separation and/or  
 CC transcription; (2) adding nucleotides (1) having a sequence  
 CC essentially complementary to the ends of (1) having a sequence  
 CC as starting points for nucleic acid synthesis and being able to act  
 CC incorporated into the amplification product; (3) amplification,  
 CC optionally with addition of other required chemical building  
 CC blocks; and (4) at least partial separation of the amplification  
 CC product into its individual strands. The method is useful for in  
 CC vitro diagnosis in human or veterinary medicine or for environmental  
 CC (eliminates the need for temperature cycling) Two primers  
 CC (AAT36954, AAT36955) were used to amplify a template molecule (AAT36956)  
 SO Sequence 41 BP; 5 A; 15 C; 14 G; 7 T; 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 17; Length 41;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20  
 Db 22 GAGCTGACTGGGTGAGGCC 3

RESULT 4

ID AAT36970 standard; DNA; 41 BP.  
 AC AAT36970;  
 DT 16-FEB-1997 (first entry)  
 DE Primer used in transcription free amplification method.  
 KW Amplification; primer; template; transcription; diagnosis;  
 KW medicine; environmental analysis; forensic analysis; ss.  
 OS Synthetic.  
 PN AT9501007-A.  
 PD 15-JUL-1996.  
 PF 13-JUN-1995; 95AT-0001007.  
 PR 13-JUN-1995; 95AT-0001007.  
 PA (HIMM) HIMMELER G.  
 DR WPI; 1996-322132/33.  
 XX Transcription free amplification of nucleic acid - with  
 XX amplification and strand sepn. of prod. at same temp.; useful for in  
 XX vitro clinical diagnosis  
 PS Example 1; Page 9; 25pp; German.  
 CC Transcription free amplification of a nucleic acid sequence (A) with  
 CC enzymes, comprises: (1) optionally, before amplification, converting  
 CC (A) at least partly to individual strands by separation and/or  
 CC transcription; (2) adding nucleotides (1) having a sequence  
 CC essentially complementary to the ends of (1) having a sequence  
 CC as starting points for nucleic acid synthesis and being able to act  
 CC incorporated into the amplification product; (3) amplification,  
 CC optionally with addition of other required chemical building  
 CC blocks; and (4) at least partial separation of the amplification  
 CC product into its individual strands. The method is useful for in  
 CC vitro diagnosis in human or veterinary medicine or for environmental  
 CC (eliminates the need for temperature cycling) Two primers  
 CC (AAT36954, AAT36955) were used to amplify a template molecule (AAT36956)  
 SO Sequence 41 BP; 5 A; 15 C; 14 G; 7 T; 0 other;



```

DT      17-FEB-1997  (first entry)
XX
DE      Oligonucleotide used in transcription free amplification method.
XX
KW      Amplification; primer; template; transcription; diagnosis;
XX      medicine; environmental analysis; forensic analysis; ss.
XX
OS      Synthetic.
XX
PN      AT9501007-A.
XX
PD      15-JUL-1996.
XX
PF      13-JUN-1995; 95AT-0001007.
XX
PR      13-JUN-1995; 95AT-0001007.
XX
PA      (HIMM)/ HIMMELER G.
XX
DP      WPI; 1996-322132/73.
XX
PT      Transcription free amplification of nucleic acid - with
XX      amplification and strand sepn. of prod. at same temp., useful for in
XX      vitro clinical diagnosis
XX
PS      Example 8; Page 20; 25pp; German.
XX
CC      Transcription free amplification of a nucleic acid sequence (A) with
XX      enzymes, comprises: (1) optionally, before amplification, converting
XX      (A) at least partly to individual strands by separation and/or
XX      transcription; (2) adding nucleotides (1) having a sequence
XX      essentially complementary to the ends of (A) and being able to act
XX      as starting points for nucleic acid synthesis and becoming
XX      incorporated into the amplification product; (3) amplification,
XX      optionally with addition of other required chemical building
XX      blocks; and (4) at least partial separation of the amplification
XX      product into its individual strands. The method is useful for in
XX      vitro diagnosis in human or veterinary medicine, or for environmental
XX      or forensic analysis. The process is simple and inexpensive
XX      (eliminates the need for temperature cycling). Four
XX      oligonucleotides (AAT36970-73) were used to amplify a template molecule
XX      (AAT36974), and generate a double stranded product using the method.
XX
SQ      Sequence 41 BP; 7 A; 14 C; 15 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 gagctgactgggtctgaagc 20
        |||||||||||||||||||
Db      20 gagctgactgggtctgaagc 39

RESULT 5
AAT36971/C
AAT36971 standard; DNA; 41 BP.
AAT36971;
AAT36971;
17-FEB-1997 (first entry)
Oligonucleotide used in transcription free amplification method.
Amplification; primer; template; transcription; diagnosis;
medicine; environmental analysis; forensic analysis; ss.
Synthetic.
AT9501007-A.
AT9501007-A.
15-JUL-1996.

```

```

XX 13-JUN-1995; 95AT-0001007.
PF 13-JUN-1995; 95AT-0001007.
XX 13-JUN-1995; 95AT-0001007.
XX (HIMM/) HIMMLER G.
PA
XX
DR WPI: 1996-322132/73.
XX
XX Transcription free amplification of nucleic acid - with
PT amplification and strand sepn. of prod. at same temp., useful for in
PR vitro clinical diagnosis
XX
PS Example 8; Page 20; 25pp; German.
XX
XX Transcription free amplification of a nucleic acid sequence (A) with
CC enzymes, comprises: (1) optionally, before amplification, converting
CC (A) at least partly to individual strands by separation and/or
CC transduction; (2) adding nucleotides (1) having a sequence
CC essentially complementary to the ends of (A) and being able to act
CC as starting points for nucleic acid synthesis and becoming
CC incorporated into the amplification product; (3) amplification,
CC optionally with addition of other required chemical building
CC blocks; and (4) at least partial separation of the amplification
CC product into its individual strands. The method is useful for in
CC vitro diagnosis in human or veterinary medicine, or for environmental
CC or forensic analysis. The process is simple and inexpensive
CC (eliminates the need for temperature cycling). Four
CC oligonucleotides (AAT36970-73) were used to amplify a template molecule
CC (AAT36974), and generate a double stranded product using the method.
XX
XX Sequence 41 BP; 5 A; 15 C; 14 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactgggtcgaagc 20
Db 22 GAGCTGACTGGGCTGCAAGGC 3
|||||
|
RESULT 6
AAT36956/C
ID AAT36956 standard; DNA; 91 BP.
XX
XX AAT36956;
AC
XX 17-FEB-1997 (first entry)
DT
XX
XX Template used in transcription free amplification method.
DE
XX
XX Amplification; primer; template; transcription; diagnosis;
KW medicine; environmental analysis; forensic analysis; ss.
XX
XX Synthetic.
OS
XX
XX AT9501007-A.
PN
XX
XX 15-JUL-1996.
PD
XX
XX 13-JUN-1995; 95AT-0001007.
PF
XX
XX 13-JUN-1995; 95AT-0001007.
PR
XX
XX (HIMM/) HIMMLER G.
PA
XX
XX WPI: 1996-322132/73.
XX
XX Transcription free amplification of nucleic acid - with
PT amplification and strand sepn. of prod. at same temp., useful for in
PR vitro clinical diagnosis

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CC homologues of any of the S.aureus DNA sequences contained on the  
 CC computer readable medium.  
 XX  
 SO Sequence 169 BP; 39 A; 51 C; 47 G; 31 T; 1 other;

Query Match 100.0%; Score 20; DB 18; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 0.87;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20  
 |||||||  
 DB 112 gagctgactgggtgaagc 131

RESULT 9  
 AAN60881/C  
 ID AAN60881 standard; DNA; 600 BP.  
 XX  
 AC AAN60881;

DE 22-OCT-1991 (first entry)

DE Sequence encoding novel polypeptide with interferon activity.

KW IFN; antitumour; antiviral; pGI-101; pGSII-102.

FT Key Location/Qualifiers  
 CDS 115..558  
 /\*tag= a

PN JP61033200-A.

PD 17-FEB-1986.

PF 22-MAY-1985; 85JP-0108299.

PR 22-MAY-1984; 84US-0613067.

PA (ASAHI) ASAHI CHEMICAL IND KK.

DR WPI: 1986-240788/37.

DR P-PSDB; AAP61073.

PT Polypeptide(s) with human immune interferon activities - obt'd. by  
 culturing transformed microbe e.g. E.coli transformed with  
 pGSII-102 (J6 17/2/86).

PS Disclosure; Page 1126; 16pp; Japanese.

CC The gene product has human immune interferon activity, excellent in  
 antitumour and antiviral treatment. The product may be expressed  
 from a suitable host eg. E.coli, transformed with plasmids pGI-101  
 or pGS-102.

SO Sequence 600 BP; 212 A; 108 C; 122 G; 158 T; 0 other;

Query Match 100.0%; Score 20; DB 7; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20  
 |||||||  
 DB 600 gagctgactgggtgaagc 581

RESULT 10  
 AAN60882/C  
 ID AAN60882 standard; DNA; 600 BP.  
 XX  
 AC AAN60882;  
 XX

DT 22-OCT-1991 (first entry)  
 XX  
 DE Sequence encoding novel polypeptide with interferon activity.  
 XX  
 KW IFN; antitumour; antiviral; pGI-101; pGSII-102.

FT Key Location/Qualifiers  
 CDS 115..558  
 /\*tag= a

PN JP61033200-A.

PD 17-FEB-1986.

PF 22-MAY-1985; 85JP-0108299.

PR 22-MAY-1984; 84US-0613067.

PA (ASAHI) ASAHI CHEMICAL IND KK.

DR WPI: 1986-240788/37.

DR P-PSDB; AAP61074.

PT Polypeptide(s) with human immune interferon activities - obt'd. by  
 culturing transformed microbe e.g. E.coli transformed with  
 pGSII-102 (J6 17/2/86).

PS Disclosure; Page 1127; 16pp; Japanese.

CC The gene product has human immune interferon activity, excellent in  
 antitumour and antiviral treatment. The product may be expressed  
 from a suitable host eg. E.coli, transformed with plasmids pGI-101  
 or pGS-102.

SO Sequence 600 BP; 213 A; 108 C; 121 G; 158 T; 0 other;

Query Match 100.0%; Score 20; DB 7; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20  
 |||||||  
 DB 600 gagctgactgggtgaagc 581

RESULT 11

AAAX0097/C  
 ID AAAX0097 standard; DNA; 710 BP.  
 XX

AC AAAX0097;

DT 12-MAY-1999 (first entry)

DE Mutated tetracycline resistance gene fragment of pBR322 clone FIND1.

KW PCR; primer; fragment; segment; insert; clone; cloning; FIND;  
 fragment inducible nucleotide diversity; DNA shuffling; antibody;  
 KW modify; tetracycline; revertant; ss.

OS Synthetic.

PN W09858080-A1.

PD 23-DEC-1998.

PF 16-JUN-1998; 98WO-GB01757.

PR 16-JUN-1997; 97GB-0012512.

PA (BIOI-) BIOINVENT INT AB.

PA (CRIP/) CRIPPS J E.

XX

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PT  Borrebaeck CMK, Ottosson RIC, Soederlund UHE;
XX  WPI: 1999-095348/08.
XX
XX  Method for generating polynucleotide sequences from a parent
XX  polynucleotide - by digesting with BAL31 then annealing and
XX  amplifying the digested fragments
XX
XX  Disclosure: Figure 6A: 55pp; English.
XX
XX  Generation of a new polynucleotide sequence or sequences from a
XX  parent polynucleotide sequence encoding one or more protein motifs
XX  comprises digesting the parent polynucleotide sequence with a
XX  restriction enzyme to generate fragments and then contacting the
XX  fragments with a template polynucleotide sequence under annealing
XX  conditions. The fragments that anneal are then amplified to
XX  generate at least one polynucleotide sequence encoding protein
XX  motifs having new or altered characteristics. The method has been
XX  designated FIND (Fragment inducible Nucleotide diversity) and
XX  provides advantages over current DNA shuffling techniques to
XX  facilitate generation of new antibodies which also can be used to
XX  derive, in an example, a tetracycline resistance gene from which they
XX  from two disrupted tetracycline genes (tetracycline sensitive
XX  phenotype). Two primers (AAK0093, AAK0094) were used initially to
XX  forward (AAK0095), or reverse (AAK0096) primer, both of which
XX  introduced a STOP codon and unique restriction site. The resulting
XX  deleted PBR322 and the resulting clones were called FIND1 with a
XX  HindIII/SalI restricted insert (AAK0097) with a 5' STOP codon which
XX  was generated using primers AAK0093 and AAK0096. The disrupted
XX  tetracycline genes were then excised and then again with restriction
XX  enzymes, and the resulting fragments were PCR amplified using
XX  primers PBR322 and the new fragments cloned back into tetracycline
XX  method. Tetracycline resistant revertants were obtained with this
XX
XX  Sequence 710 BP: 113 A: 228 C: 210 G: 159 T: 0 other;
XX
XX  Query Match
XX  Best Local Similarity 100.0%; Score 20; DB 20; Length 710;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 gagctgactgggttaagc 20
XX  DB 461 GAGCTGACTGCGTTGAGGC 442
XX
XX  RESULT 12
XX  AA234980/c
XX  ID AA234980 standard; cDNA; 1097 BP.
XX  AC AA234980;
XX  DT 28-FEB-2000 (first entry)
XX  DE Mouse F1Z21 expression construct.
XX  KW m-F1Z21; F1Z2; found in inflammation zone; mouse; neurotrophin;
XX  inhibitor; neuropathy; AIDS; impotence; hyperextension; pain; asthma;
XX  cystitis; bowel disease; cardiac arrhythmia; sudden cardiac death;
XX  vasogenic edema; encephalitis; infection; HIV; cancer; therapy;
XX  vector; pST31-F1Z21; ds.
XX
```

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OS  Chimeric - Mus musculus.
XX  Chimeric - synthetic.
XX
XX  Key
XX  CDS
XX  sig_peptide 309..638
XX  FT /tag= a
XX  FT 309..371
XX  FT mat_peptide 372..635
XX  FT /tag= b
XX  PN M0955868-A2.
XX
XX  PD 04-NOV-1999.
XX
XX  PF 20-APR-1999; 99MO-US08615.
XX
XX  PR 24-APR-1998; 98US-0082999.
XX  PR 12-MAY-1998; 98US-0085149.
XX  PR 14-SEP-1998; 98US-0100263.
XX
XX  PA (GETH ) GENENTECH INC.
XX
XX  PI Gurney AL, Hebert C, Henzel WJ, Kabakoff R, Shelton DL, Tumas DB;
XX  WPI: 2000-062031/05.
XX  DR P-PSDB; AAY32327.
XX
XX  PT New treatment of a neurotrophin action-associated condition using F1Z2
XX  protein
XX
XX  PS Example 2, Fig 6: 61pp; English.
XX
XX  CC This is the nucleotide sequence the F1Z2 expression construct in
XX  CC vector pST31-F1Z21. The construct includes a coding region for
XX  CC a (His)8-tagged F1Z2 mature protein (see also AAY32328)
XX  CC and was designed for expression of m-F1Z21 (see also AAY32328)
XX  CC m-F1Z21 is a member of a new family of secreted proteins that are
XX  CC capable of inhibiting the actions of neurotrophins on responsive
XX  CC neurons. Mature F1Z2 proteins and their agonists and antagonists
XX  CC are used in claimed methods of treating pathologic conditions
XX  CC associated with neurotrophin action.
XX
XX  Sequence 1097 BP: 275 A: 274 C: 265 G: 281 T: 2 other;
XX
XX  Query Match
XX  Best Local Similarity 100.0%; Score 20; DB 21; Length 1097;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 gagctgactgggttaagc 20
XX  DB 945 GAGCTGACTGCGTTGAGGC 926
XX
XX  RESULT 13
XX  AA235503/c
XX  ID AA235503 standard; cDNA; 1130 BP.
XX  AC AA235503;
XX  DT 24-JAN-2000 (first entry)
XX  DE Clone ATC 5 polynucleotide sequence, encoding bovine ACS.
XX  KW bovine acetyl coenzyme A synthetase; ACS; milk production; lactation;
XX  Holstein mammary gland tissue; ATR; ATC 5; ss.
XX  OS Bos sp.
XX
XX  Key
XX  CDS
XX  Location/Qualifiers
XX  FT 1..1130
XX  FT /*tag= a
XX
```

FT	/product= ACS
FT	/note= "Acetyl coenzyme A synthetase, this sequence
FT	contains 2 in frame stop codons"
FT	/transl_except- (Pos:46..48, aa:Xaa)
FT	/transl_except- (Pos:130..132, aa:Xaa)
FT	/transl_except- (Pos:349..351, aa:Xaa)
FT	/transl_except- (Pos:472..474, aa:Xaa)
FT	/transl_except- (Pos:525..527, aa:Xaa)
FT	/transl_except- (Pos:784..786, aa:Xaa)
FT	/transl_except- (Pos:805..807, aa:Xaa)
FT	/transl_except- (Pos:847..489, aa:Xaa)
FT	/transl_except- (Pos:868..879, aa:Xaa)
FT	/note= "Xaa = unknown"
XX	
PN	US5981187-A.
XX	
PD	09-NOV-1999.
XX	
PX	26-AUG-1997; 97US-0918966.
PR	08-MAR-1996; 96US-0613965.
PA	(UNMS ) UNIV MICHIGAN STATE.
PI	Raafat AM, Cook RM;
XX	
DR	WPI; 1999-633309/54.
DR	P-PsDB; AAY52098.
PT	Determining potential milk production in calves -
PS	Example 1; Fig 26A; 41pp; English.
CC	This is the clone ATC 5 nucleotide sequence isolated using AR8 cDNA
CC	(AAZ3501-z35502: partial ACS sequences) from bovine mammary gland
CC	tissue. The sequence is thought to encode bovine acetyl coenzyme A
CC	synthetase (ACS). AR8 sequences were isolated via screening with rabbit
CC	anti-ACS sera. ACS is involved in the synthesis of acetyl coenzyme A
CC	which is a major substrate for milk synthesis and occupies a central
CC	position in the metabolism of Holstein mammary gland tissue. ACS activity
CC	is directly related to milk production. The AR8 sequences are used in a
CC	method for determining the potential milk production potential in calves
CC	before milk production and breeding begins. The method involves
CC	determining the level of ACS or mRNA encoding ACS in the mammary tissue
CC	of a calf, which allows an estimation of the milk production potential of
CC	a calf. The method can be used in selection and/or breeding programmes to
CC	enhance milk production and to identify cows which may be in need of
CC	treatment to augment lactation.
SO	Sequence 1130 BP; 198 A; 351 C; 305 G; 268 T; 8 other;
OY	Query Match 100.0%; Score 20; DB 20; Length 1130;
ID	Best Local Similarity 100.0%; Pred. No. 1.1;
XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 gagctgactgggttgaagc 20
ID	
DB	836 GAGCTGACTGGGTGAAGC 817
RESULT 14	
AAZ87413/C	
AAZ87413 standard; cDNA; 1130 BP.	
AAZ87413;	
22-May-2000 (first entry)	
Bovine acetyl coenzyme A synthetase (ACS) cDNA clone ATC5.	
Acetyl coenzyme A synthetase; ACS; bovine; acetyl CoA; lactation;	
fusion protein; beta-galactosidase; antibody; affinity purification;	

KM	breeding programme; milk production; selection; clone ATC5; ss.
OS	Bos taurus var. Holstein.
XH	
XX	Location/Qualifiers
FT	Key
FT	CDS
FT	220..1130
FT	/tag= a
FT	/partial
FT	/product- "Bovine acetyl coenzyme A synthetase (ACS)"
FT	/note- "No stop codon given in the specification"
FT	/transl_except- (pos:349..351, aa:Xaa)
FT	/transl_except- (pos:472..474, aa:Xaa)
FT	/transl_except- (pos:523..525, aa:Xaa)
FT	/transl_except- (pos:784..786, aa:Xaa)
FT	/transl_except- (pos:805..807, aa:Xaa)
FT	/transl_except- (pos:847..849, aa:Xaa)
FT	/transl_except- (pos:868..870, aa:Xaa)
FT	/note- "Xaa is unknown"
PN	US6013496-A.
PD	11-JAN-2000.
XX	
PE	26-AUG-1997; 97US-0921655.
PR	08-MAR-1996; .96US-0613965.
PA	(UNMS ) UNIV MICHIGAN STATE.
PI	Cook RM, Raafat AM;
DR	WPI: 2000-170260/15.
DR	P-PDB: AAY77268.
PT	New isolated acetyl coenzyme A synthase (ACS) fusion proteins, for affinity purification of anti-ACS antibodies which are used to identify cows with high milk production potential -
PS	Claim 1; Fig 26A; 50pp: English.
XX	
CC	The invention relates to fusion proteins comprising bovine acetyl coenzyme A synthetase (ACS), and to nucleotide sequences encoding the proteins. ACS catalyses the acetate activation reaction, which generates acetyl CoA. Acetyl CoA is a major substrate for milk synthesis, and ACS activity is directly correlated with milk production. The fusion protein of the invention is either a beta-galactosidase/ACS fusion protein in which the ACS component is encoded by DNA (AAZ87413) present in plasmid pUC19-PARC (ATCC 98008) or a fusion protein in which the ACS component is encoded by DNA (AAZ87415-287416) present in plasmid pUC19-PAR8 (ATCC 209191). cDNA was produced via reverse transcription from poly(A)+ RNA isolated from bovine mammary tissue taken at peak lactation. The cDNAs were cloned into the EcoRI site of lambda phage gtl1, producing beta-galactosidase/cDNA fusion genes, and the phage library screened with polyclonal rabbit anti-bovine ACS antibodies produced against purified bovine (Holstein) ACS. A positive plaque, lambda AR8, was identified and the cDNA insert (cloned into pUC13) sequenced. Lambda AR8 was also used to infect Escherichia coli, in order to produce beta-galactosidase/ACS fusion protein for assay of ACS activity. An AR8 probe was used to rescreen the bovine mammary gland cDNA phase library, and another positive plaque identified (lambda ATC5). The ATC5 insert was cloned into pUC19 and sequenced, and the ACS fusion protein activity assayed. The fusion proteins of the invention may be used for affinity purification of rabbit anti-ACS antibodies. The antibodies are used to determine levels of ACS in bovine mammary tissue, particularly to identify cows with potential for high level milk production in breeding programmes. Anti-ACS antibodies, affinity purified with ACS fusion protein allow calves with high levels of ACS (indicating potential for high level milk production, and therefore preferred for breeding) to be identified. This means that relatively fewer animals need to be bred, and selection of animals for high level ACS production will result in significant increases in milk production. The present sequence represents the bovine ACS cDNA clone ATC5.

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XX
SQ Sequence 1130 BP: 198 A; 351 C; 305 G; 268 T; 8 other;

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 1130;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20
DB 836 GAGCTGACTGCGTTGAAGC 817

RESULT 15
AAQ27876/C
ID AAQ27876 standard; DNA; 1140 BP.
AC AAQ27876;
DT 08-FEB-1993 (first entry)
DE Ricin A gene from PIC1102.
KW pH; temperature; cultivation; host; soluble; ss.
OS Synthetic.
FX
FH Key
FT Promoter
FT Location/Qualifiers
FT 1..89
FT /tag= a
FT /note= "region indicated in the specification as
FT 90..92 comprising a TTP promoter, S-D and IDS"
FT /tag= b
FT /label= translation_initiation_codon
FT /note= "first translation initiation codon out of
FT 129..131 frame with that of Ricin A coding region"
FT /tag= c
FT /label= stop_codon
FT /note= "in-frame termination codon prior to the
FT 132..135 ricin A initiation codon"
FT /tag= d
FT /note= "SD capable of re-initiating translation
FT 143..946
FT /tag= e
FT /label= ricin_A
FT 947..1140
FT /tag= f
FT /note= "region comprising terminator"

EP501692-A.
XX
PN 02-SEP-1992.
XX
XX 21-FEB-1992; 92EP-0301466.
XX
PR 26-FEB-1991; 91GB-0003925.
PR 26-FEB-1991; 91GB-0003926.
XX 26-FEB-1991; 91GB-0004016.
PA (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Filton JE, Hockney RC, Kara BV;
XX WPI: 1992-294124/36.
XX P-PSDB; AAR30722.
XX
PT Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by
PT adjusting pH and/or temp. during cultivation to increase yield of
PT soluble prod.
PT
```

```

XX
XX Disclosure: Fig 9, 49pp; English.
XX
CC Prepn. of ricin A comprises cultivating a host, including a DNA
CC sequence which encodes ricin A, e.g. from PIC1102, in a nutrient
CC medium for an initial period at a first pH value which favours growth
CC of the host; and cultivation the host to a further period at a pH
CC lower than the first pH value, and optionally harvesting the host during the
CC terminal portion of the cultivation and harvesting the host during the
CC cultivation of hosts, high yields of soluble recombinant ricin A
CC are obtained.
XX
SQ Sequence 1140 BP: 319 A; 256 C; 248 G; 317 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 20; DB 13; Length 1140;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggtgaagc 20
DB 1076 GAGCTGACTGCGTTGAAGC 1057

Search completed: December 13, 2001, 15:43:09
Job time: 8183 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:34:38 ; Search time 1854.2 Seconds  
(without alignments)  
177.944 Million cell updates/sec

Title: US-09-631-709-2

Perfect score: 20  
Sequence: 1 gagctgactggttgtaagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_com:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
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11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
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21: em\_or:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_inv:\*  
32: em\_htgo\_rnd:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	6	AX137658	AX137658 Sequence
2	20	100.0	41	6	A58755	A58755 Sequence 1
3	20	100.0	91	6	A58757	A58757 Sequence 3
4	20	100.0	91	6	A58758	A58758 Sequence 4
5	20	100.0	162	1	NGSIPUB	X60747 N.gonorrhoe
6	20	100.0	600	6	E00695	E00695 A plasmid p
7	20	100.0	710	6	A81874	A81874 Sequence 5
8	20	100.0	710	6	AR120677	AR120677 Sequence
9	20	100.0	1050	6	100073	100073 Sequence 2
10	20	100.0	1130	6	AR084610	AR084610 Sequence
11	20	100.0	1138	1	EC019114	Y19114 Escherichia
12	20	100.0	1140	6	A23903	A23903 partial seq
13	20	100.0	1140	6	AR059851	AR059851 Sequence
14	20	100.0	1140	6	AR059851	125094 Sequence 15
15	20	100.0	1489	10	AF128236	AF128236 Mus muscu
16	20	100.0	1518	10	MMCEA4B	AF128236 Mus muscu
17	20	100.0	1842	10	AF113598	AF113598 Mus muscu
18	20	100.0	1878	10	MMCEA4A	AF113598 Mus muscu
19	20	100.0	2043	10	MUSPGGLYD	X98111 M.musculus
20	20	100.0	2538	12	ASPMIN1	M83344 Mouse pregn
21	20	100.0	2646	12	ASPMIN3	Z50148 Artificial
22	20	100.0	3273	12	ARP327	Z50149 Artificial
23	20	100.0	3274	12	SYNBR327V	V00083 Artificial
24	20	100.0	3302	6	A20357	L08856 pBR327 cion
25	20	100.0	3302	6	A20358	A20357 plasmid pTG
26	20	100.0	3327	6	AX138937	A20358 plasmid pTG
27	20	100.0	3369	6	AX138929	AX138937 Sequence
28	20	100.0	3423	6	A99078	AX138929 Sequence
29	20	100.0	3474	6	A28084	A99078 Sequence 86
30	20	100.0	3474	6	A28085	A28084 pMTNF-MPH p
31	20	100.0	3474	6	A75741	A28085 pMTNF-MPH p
32	20	100.0	3474	6	AR085100	A75741 Sequence 10
33	20	100.0	3658	12	SYNPAR153V	AR085100 Sequence
34	20	100.0	3668	12	SYNBR327P	L08857 pAT153 cion
35	20	100.0	3773	12	SYNPM7551V	L08857 pBR327par c
36	20	100.0	3779	12	SYNPM7571V	L09154 pMT551 expr
37	20	100.0	3809	12	SYNPM7511V	L09155 pMT551 expr
38	20	100.0	3903	12	PURD158	L09153 pMT551 expr
39	20	100.0	3903	12	SYNJRDI58V	X01453 Plasmid vec
40	20	100.0	3913	12	EVU51557	L08919 pURD158 cion
41	20	100.0	3930	12	SYNPM7RS3V	U51557 Expression
42	20	100.0	3954	6	AX138934	L08955 pTRS3 cion1
43	20	100.0	3976	6	AX138930	AX138934 Sequence
44	20	100.0	4006	12	SYNPKTH606	AX138930 Sequence
45	20	100.0	4009	6	A39734	L08928 pKTH606 cion

## ALIGNMENTS

RESULT 1  
AX137658  
LOCUS AX137658 20 bp DNA  
DEFINITION Sequence 2 from Patent EP1076096.  
ACCESSION AX137658  
VERSION AX137658.1 GI:14273843  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Koizumi,S., Nagano,H., Endo,T., Tabata,K. and Ozaki,A.  
TITLE Process for producing gdp-fucose  
JOURNAL Patent: EP 1076096-A 2 14-FEB-2001;  
KYOMA HAKKO KOGYO CO., LTD. (JP)  
FEATURES  
source location/Qualifiers  
1..20  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Synthetic DNA"

PAT 30-MAY-2001

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Page 2

BASE COUNT 4 a 3 c 9 g 4 t  
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 6; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaagc 20  
Db 1 gagctgactgggttgaagc 20

RESULT 2

LOCUS A58755 41 bp DNA  
DEFINITION Sequence 1 from Patent WO9700330.  
ACCESSION A58755  
VERSION A58755.1 GI:3714292  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS  
HIMMLER GOTTFRIED (AT) 03-JAN-1997;  
Other publication AU 5887296 970115  
Other publication AT 402203 970325  
Other publication AT 100795 960715.  
Location/Qualifiers  
1. .41  
/organism="unidentified"

BASE COUNT 5 a 15 c 14 g 7 t  
ORIGIN

Query Match

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaagc 20  
Db 22 gagctgactgggttgaagc 3

RESULT 3

LOCUS A58757 91 bp DNA  
DEFINITION Sequence 3 from Patent WO9700330.  
ACCESSION A58757  
VERSION A58757.1 GI:3714294  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS  
HIMMLER GOTTFRIED (AT) 03-JAN-1997;  
Other publication AU 5887296 970115  
Other publication AT 402203 970325  
Other publication AT 100795 960715.  
Location/Qualifiers  
1. .91  
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BASE COUNT 13 a 29 c 31 g 18 t  
ORIGIN

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Best Local Similarity 100.0%; Score 20; DB 6; Length 91;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagcgcactgggttgaagc 20  
Db 22 gagcgcactgggttgaagc 3

RESULT 4

LOCUS A58758 91 bp DNA  
DEFINITION Sequence 4 from Patent WO9700330.  
ACCESSION A58758  
VERSION A58758.1 GI:3714295  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS  
HIMMLER GOTTFRIED (AT) 03-JAN-1997;  
Other publication AU 5887296 970115  
Other publication AT 402203 970325  
Other publication AT 100795 960715.  
Location/Qualifiers  
1. .91  
/organism="unidentified"

BASE COUNT 13 a 29 c 31 g 18 t  
ORIGIN

Query Match

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Oy 1 gagcgcactgggttgaagc 20  
Db 22 gagcgcactgggttgaagc 3

RESULT 5

LOCUS NGSP11B 162 bp DNA  
DEFINITION N.gonorrhoeae NG-18 silent pilin gene. BCT  
ACCESSION X60747  
VERSION X60747.1 GI:44986  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Submitted (26-JUN-1991) R. Haas, Max-Planck-Institut fuer Biologie,  
Abteilung Interklimatologie, Spemannstrasse 34, D-7400 Tuebingen,  
FRG  
See X60745, X60747-X60751 for related sequences.  
Location/Qualifiers  
1. .162  
/organism="Neisseria gonorrhoeae"

BASE COUNT 13 a 29 c 31 g 18 t  
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QY      1 gagctgactggtgaagc 20
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Db      62 GAGCTGACTGGTTGAGGC 43

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RESULT	6
E00695/c	
LOCUS	E00695 600 bp RNA PAT 29-SEP-1997
DEFINITION	A plasmid pGSII-102 containing a DNA encoding a polypeptide having human gamma-interferon activities.
ACCESSION	E00695
VERSION	E00695.1 GI:2168972
KEYWORDS	UP 1986033200-A/1.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

ORGANISM	REFERENCE	AUTHORS	JOURNAL	COMMENT
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 600)				
Takahashi, Y., Tsuchi, M., Chikazuru, T. and Jiyon, R.				
GAMMA-INTERFERON				
Patent: JP 1986033200-A 1 17-FEB-1986;				
ASAHII CHEM IND CO LTD				
OS Homo sapiens				

PD 17-FEB-1986  
PF 22-MAY-1985 JP 1985108299  
PR 22-MAY-1984 US 84 613067  
PI TAKAHASHI YASUYUKI, TAUCHI MASATOSHI, CHIYARAUDU TOTSUO, PI  
JIYON ROTOSHI  
PC COTK15/26,A61K45/02,C12N1/20,C12N15/00,C12P1/02,(C12N1/20,  
C12R1/19),  
(C12N15/00,C12R1:19),(C12P1/02,C12R1:19);

	FH	Key	location/Qualifiers	,	
	FH	CDS	115..558	/product='polypeptide having human	FT
	FT		gamma-interferon		
	FT		activities'		
	FT	mat_peptide	115..555	/product='polypeptide having human	FT
	FT		gamma-interferon		
	FT		activities'		
	FT	variation	replace(536,'A').		
	FT		location/Qualifiers		
			1..600		
			/organism="Homo sapiens"		
			/db_xref="taxon:9606"		
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source					
BASE COUNT		212 a	108 c	122 g	158 t
ORIGIN					

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Best Local Similarity	100.0%;	Pred. No. 7;		

	Matches	20; Conservative	0; Mismatches	0; Indels	0; Gaps
Qy	1	gagctgactggttgaagc	20		
Db	600	GAGCTGACTGGTTGAAGC	581		

RESULT	7				21-JAN-2006
AB1874/c					
LOCUS	AB1874	710 bp	DNA	circular	PAT
DEFINITION	Sequence	5 from Patent	WO9858080.		
ACCESSION	AB1874				
VERSION	AB1874.1	GI:5731888			

ORGANISM	unidentified unclassified, 1 (bases 1 to 710)
REFERENCE	Soederlind,U.H. and Borrebaeck,C.A.
AUTHORS	A METHOD FOR IN VITRO MOLECULAR EVOLUTION OF PROTEIN FUNCTION
TITLE	Patent: WO 9858080-A 5 23-DEC-1998;
JOURNAL	

BASE COUNT	113 a	228 c	210 g	159 t
ORIGIN	/organism="unidentified" /db_xref="taxon:32644"			

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Best Local Similarity	100.0%	Pred. No. 7;		
Matches 20; Conservative	0;	Mismatches	0;	Gaps 0;

Qy 1 gagctgactggttgagc 20  
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 Db 461 GAGCTGACTGCCCTTGAAGGC 442

RESULT	8		PAT	16-MAY-2001
ARI20677/c				
LOCUS	ARI20677	710 bp	DNA	
DEFINITION	Sequence 5 from patent US 6159690.			
ACCESSION	ARI20677			
VERSION	ARI20677.1	GI:14104253		

REFERENCE	1 (bases 1 to 710)
AUTHORS	Borrebaeck,C.Arnekrister, Soderlund,U.Hansekl and Ottosson,R.ingridcamilla,
TITLE	Method for in vitro molecular evolution of protein function using exonuclease and amplification
JOURNAL	Patent: US 6159690-A 5 12-Dec-2000;
FEATURES	Location/Qualifiers
source	1..710
BASE COUNT	113 a 228 c 210 g 159 t
ORIGIN	1..organism="unknown"

Query	March		100.0%	Score	20;	DB	6;	Length	710;
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Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

  

QY	1	gagctactgggttcgaagc	20
db	461	GAGCTGACTGGGTTCGAAGC	442

RESULT 9  
I00073/c

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Page 4

LOCUS 100073 1050 bp ss-DNA  
DEFINITION Sequence 2 from Patent US 4921698.  
ACCESSION 100073  
VERSION 100073.1 GI:313995  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1050)  
AUTHORS Shirai, T. and Wallace, R. Bruce.  
TITLE Polypeptide having gamma-interferon activity lacking amino acids  
JOURNAL Patent: US 4921698-A 2 01-MAY-1990;  
Asahi Kasei Kogyo Kabushiki Kaisha;  
Osaka, ;  
JP;  
COMMENT On Jul 30, 1993 this sequence version replaced gi:285533.  
FEATURES  
source location/Qualifiers  
BASE COUNT 347 a 210 c 165 g 328 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 20; DB 6; Length 1050;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1043 GAGCTGACTGGGTGAAGC 1024  
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1 gagctgactgggttgaagc 20  
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RESULT 10  
LOCUS AR084610 1130 bp DNA  
DEFINITION Sequence 1 from Patent US 5981187.  
ACCESSION AR084610  
VERSION AR084610.1 GI:10011381  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1130)  
AUTHORS Cook, R.M. and Raaijmakers, A.M.  
TITLE Selection method involving acetal coenzyme a synthetase in calves  
JOURNAL Patent: US 5981187-A 1 09-NOV-1999;  
FEATURES  
source location/Qualifiers  
BASE COUNT 198 a 350 c 306 g 268 t 8 others  
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Best Local Similarity 100.0%; Score 20; DB 6; Length 1130;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 836 GAGCTGACTGGGTGAAGC 817  
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RESULT 11  
LOCUS ECO19114 1138 bp DNA  
DEFINITION Escherichia coli partial plasmid tetracycline resistance gene for tetracycline  
ACCESSION Y19114  
VERSION Y19114.1 GI:12053581  
KEYWORDS tetr gene; tetracycline resistance.  
SOURCE Escherichia coli.  
ORGANISM Escherichia coli

REFERENCE 1 (bases 1 to 1138)  
AUTHORS Frech, G. and Schwarz, S.  
JOURNAL unpublished  
REFERENCE 2 (bases 1 to 1138)  
AUTHORS Schwarz, S.P.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUN-1999) S.P. Schwarz, Inst. fuer Tierzucht und  
Tierverhalten, FAL, Doernbergstr. 25-27, 29223 Celle, GERMANY  
FEATURES  
source location/Qualifiers  
1. 1138  
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GSLAIVTSITSTISPLVTAIVAAASASTWNGLMIVGALVIVCL"  
BASE COUNT 181 a 363 c 336 g 258 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 20; DB 1; Length 1138;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 596 GAGCTGACTGGGTGAAGC 577  
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1 gagctgactgggttgaagc 20  
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RESULT 12  
LOCUS A23903 1140 bp DNA  
DEFINITION Partial sequence of pIC1102.  
ACCESSION A23903  
VERSION A23903.1 GI:641803  
KEYWORDS  
SOURCE Synthetic construct.  
ORGANISM Artificial construct.  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Baril, P.T.  
TITLE Vector.  
JOURNAL Patent: EP 0502637-A 60 09-SEP-1992;  
IMPERIAL CHEMICAL INDUSTRIES PLC  
FEATURES  
source location/Qualifiers  
1. 1140  
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BASE COUNT 319 a 256 c 248 g 317 t  
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Query Match 100.0%; Score 20; DB 6; Length 1140;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 13  
LOCUS AR059851 1140 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 60 from patent US 5840521.  
ACCESSION AR059851  
VERSION AR059851.1 GI:5986301  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Barth,P,Thomas.  
TITLE Expression vector containing an inducible selection gene system  
JOURNAL Patent: US 5840521-A 60 24-NOV-1998;  
FEATURES  
source 1.1140  
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BASE COUNT 319 a 257 c 248 g 316 t  
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 7;  
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QY 1 gagctgactggtgaagc 20  
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Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 14  
LOCUS I25094 1140 bp DNA PAT 07-OCT-1996  
DEFINITION Sequence 15 from patent US 5547867.  
ACCESSION I25094  
VERSION I25094.1 GI:1604964  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Kara,B.V., Hockney,R.C. and Fitton,J.F.  
TITLE Fermentation processes for preparing soluble ricin A  
JOURNAL Patent: US 5547867-A 15 20-AUG-1996;  
FEATURES  
source 1.1140  
/organism="unknown"

Query Match 100.0%; Score 20; DB 6; Length 1140;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggtgaagc 20  
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Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 15  
AF128236/c 1489 bp mRNA ROD 31-OCT-1999  
LOCUS Mus musculus pregnancy specific glycoprotein 18 mRNA, complete cds.  
DEFINITION AF128236  
ACCESSION AF128236  
VERSION AF128236.1 GI:6164607  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1489)  
AUTHORS Drexler,G.S., Wessells,J. and Zimmermann,W.  
TITLE PSG 18 induces IL-10 in murine macrophages  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1489)  
AUTHORS Drexler,G.S., Wessells,J. and Zimmermann,W.  
TITLE Direct Submission  
JOURNAL Submitted (12-FEB-1999) Pathology, Uniformed Services University of  
the Health Sciences, 4301 Jones Bridge Rd., Bethesda, MD 20814, USA  
FEATURES  
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/db\_xref="GI:6164608"

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BASE COUNT 423 a 368 c 335 g 363 t  
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 1489;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: December 13, 2001, 15:34:40  
Job time: 7674 sec

Fri Dec 14 09:21:15 2001

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